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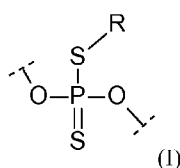
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(54) Title: OLIGONUCLEOTIDES COMPRISING A PHOSPHORODITHIOATE INTERNUCLEOSIDE LINKAGE



(57) Abstract: The present invention relates to an oligonucleotide comprising at least one phosphorodithioate internucleoside linkage of formula (I) (I) as defined in the description and in the claim. The oligonucleotide of the invention can be used as a medicament.



Oligonucleotides comprising a phosphorodithioate internucleoside linkage

BACKGROUND

The use of synthetic oligonucleotides as therapeutic agents has witnessed remarkable progress over recent decades leading to the development of molecules acting by diverse mechanisms including RNase H activating gapmers, splice switching oligonucleotides, microRNA inhibitors, siRNA or aptamers (S. T. Crooke, *Antisense drug technology: principles, strategies, and applications*, 2nd ed. ed., Boca Raton, FL: CRC Press, **2008**). However, oligonucleotides are inherently unstable towards nucleolytic degradation in biological systems. Furthermore, they show a highly unfavorable pharmacokinetic behavior. In order to improve on these drawbacks a wide variety of chemical modifications have been investigated in recent decades. Arguably one of the most successful modification is the introduction of phosphorothioate linkages, where one of the non-bridging phosphate oxygen atoms is replaced with a sulfur atom (F. Eckstein, *Antisense and Nucleic Acid Drug Development* **2009**, *10*, 117-121.). Such phosphorothioate oligodeoxynucleotides show an increased protein binding as well as a distinctly higher stability to nucleolytic degradation and thus a substantially higher half-life in plasma, tissues and cells than their unmodified phosphodiester analogues. These crucial features have allowed for the development of the first generation of oligonucleotide therapeutics as well as opened the door for their further improvement through later generation modifications such as Locked Nucleic Acids (LNAs). Replacement of a phosphodiester linkage with a phosphorothioate, however, creates a chiral center at the phosphorous atom. As a consequence, all approved phosphorothioate oligonucleotide therapeutics are used as mixtures of a huge amount of diastereoisomeric compounds, which all potentially have different (and possibly opposing) physiochemical and pharmacological properties.

While the stereospecific synthesis of single stereochemically defined phosphorothioate oligonucleotides is now possible (N. Oka, M. Yamamoto, T. Sato, T. Wada, *J. Am. Chem. Soc.* **2008**, *130*, 16031-16037) it remains a challenge to identify the

stereoisomer with optimal properties within the huge number of possible diastereoisomers. In this context, the reduction of the diastereoisomeric complexity by the use of non-chiral thiophosphate linkages is of great interest. For example, the symmetrical non-bridging dithioate modification (see e.g. W. T. Wiesler, M. H. Caruthers, *J. Org. Chem.* **1996**, *61*, 4272-4281), where both non-bridging oxygen atoms within the phosphate linkage are replaced by sulfur has been applied to immunostimulatory oligonucleotides (A. M. Krieg, S. Matson, E. Fisher, *Antisense Nucleic Acid Drug Dev.* **1996**, *6*, 133-139), siRNA (e.g. X. Yang, M. Sierant, M. Janicka, L. Peczek, C. Martinez, T. Hassell, N. Li, X. Li, T. Wang, B. Nawrot, *ACS Chem. Biol.* **2012**, *7*, 1214-1220) and aptamers (e.g. X. Yang, S. Fennewald, B. A. Luxon, J. Aronson, N. K. Herzog, D. G. Gorenstein, *Bioorg. Med. Chem. Lett.* **1999**, *9*, 3357-3362). Interestingly, attempts to make use of this non-chiral modification in the context of antisense oligonucleotides have met with limited success to date (see e.g. M. K. Ghosh, K. Ghosh, O. Dahl, J. S. Cohen, *Nucleic Acids Res.* **1993**, *21*, 5761-5766. and J. P. Vaughn, J. Stekler, S. Demirdji, J. K. Mills, M. H. Caruthers, J. D. Iglehart, J. R. Marks, *Nucleic Acids Res.* **1996**, *24*, 4558-4564).

To our surprise we have now found that non-bridging phosphorodithioates can be introduced into oligonucleotide, in particular to oligonucleotide gapmers or mixmers in general and LNA-DNA-LNA gapmers or LNA/DNA mixmers in particular. The modification is well tolerated and the resulting molecules show great potential for therapeutic applications, while every non-bridging phosphorodithioate modification reduces the size of the overall library of possible diastereoisomers by 50%. When the modification is placed in the LNA flanks of gapmers, the resulting oligonucleotides turn out to be generally more potent than the corresponding all-phosphorothioate parent. In general, the modification is additionally well tolerated within the gap region and even more surprisingly can lead to an improved potency as well, when positioned appropriately.

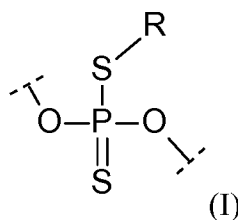
We have thus surprisingly found that the invention provides oligonucleotides with improved physiochemical and pharmacological properties, including, for example, improved potency. In some aspects, the oligonucleotide of the invention retains the activity or efficacy, and may be as potent or is more potent, than the identical compound where the phosphodithioate linkages of formula (IA or IBIB) are replaced with the conventional stereorandom phosphorothioate linkages (phosphorothioate reference compound). Every introduction of the non-bridging phosphorodithioate modification removes one of the chiral centers at phosphorous and thereby reduces the diastereoisomeric complexity of the compound by 50%. Additionally, whenever a dithioate modification is introduced, the oligonucleotide appears to be taken up dramatically better into cells, in particular into hepatocytes, muscle cells, heart cells for example.

The introduction of non-bridging dithioate modifications into the LNA flanks of gapmers appears to be particularly beneficial, leading to molecules demonstrating a higher target reduction and a substantially better uptake behavior, higher stability and good safety profile.

- 5 The chemical synthesis of non-bridging phosphorodithioate linkages in oligonucleotides is best achieved by solid phase oligonucleotide synthesis techniques using appropriate thiophosphoramidite building blocks. The successful application of such thiophosphoramidites has been described for regular DNA (X. Yang, *Curr Protoc Nucleic Acid Chem* **2016**, 66, 4.71.71-74.71.14.) as well as RNA (X. Yang, *Curr Protoc Nucleic*
10 *Acid Chem* **2017**, 70, 4.77.71-74.77.13.) and the required building blocks are available from commercial sources. Interestingly, the more challenging synthesis of the corresponding LNA thiophosphoramidites has not been reported. Within this application, we also report the successful synthesis of all four LNA thiophosphoramidites and their incorporation into oligonucleotides.

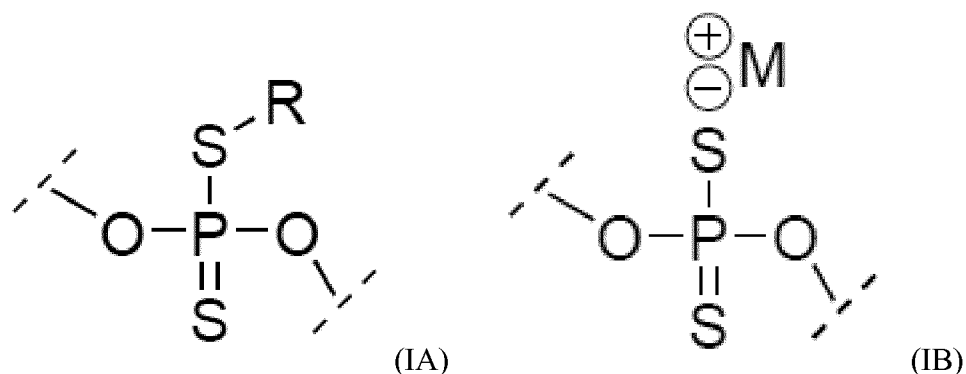
15 STATEMENT OF THE INVENTION

The invention relates to an oligonucleotide comprising at least one phosphorodithioate internucleoside linkage of formula (I)



- 20 wherein one of the two oxygen atoms is linked to the 3' carbon atom of an adjacent nucleoside (A¹) and the other one is linked to the 5' carbon atom of another adjacent nucleoside (A²), wherein at least one of the two nucleosides (A¹) and (A²) is a LNA nucleoside and wherein R is hydrogen or a phosphate protecting group. The invention further relates in particular to a gapmer oligonucleotide comprising a phosphorodithioate internucleoside linkage of formula (I). The invention also relates to a process for the
25 manufacture of an oligonucleotide according to the invention and to a LNA nucleoside monomer useful in particular in the manufacture of an oligonucleotide according to the invention.

The invention relates to an oligonucleotide comprising at least one phosphorodithioate internucleoside linkage of formula (IA) or (IB)



wherein one of the two oxygen atoms is linked to the 3' carbon atom of an adjacent nucleoside (A¹) and the other one is linked to the 5' carbon atom of another adjacent nucleoside (A²), and wherein in (IA) R is hydrogen or a phosphate protecting group, and
 5 in (IB) M⁺ is a cation, such as a metal cation, such as an alkali metal cation, such as a Na⁺ or K⁺ cation; or M⁺ is an ammonium cation.

Alternatively stated M is a metal, such as an alkali metal, such as Na or K; or M is NH₄.

The invention provides an antisense oligonucleotide comprising a
 10 phosphorodithioate internucleoside linkage, of formula IA or IB as described herein. The oligonucleotide of the invention is preferably a single stranded antisense oligonucleotide, which comprises one or more 2' sugar modified nucleosides, such as one or more LNA nucleosides or one or more 2' MOE nucleosides. The antisense oligonucleotide of the invention is capable of modulating the expression of a target nucleic acid, such as a target
 15 pre-mRNA, or target microRNA in a cell which is expressing the target RNA – in vivo or in vitro. In some embodiments, the single stranded antisense oligonucleotide further comprises phosphorothioate internucleoside linkages. The single stranded antisense oligonucleotide may, for example may be in the form of a gapmer oligonucleotide, a mixmer oligonucleotide or a totalmer oligonucleotide. The single stranded antisense
 20 oligonucleotide mixmer may be for use in modulating a splicing event in a target pre-mRNA. The single stranded antisense oligonucleotide mixmer may be for use in inhibiting the expression of a target microRNA.

The invention further refers to the use of the oligonucleotide of the invention, such as the single stranded antisense oligonucleotide as a therapeutic.

25 The invention further relates in particular to a mixmer oligonucleotide comprising a phosphorodithioate internucleoside linkage of formula (IA or IB). The invention further relates in particular to a totalmer oligonucleotide comprising a phosphorodithioate internucleoside linkage of formula (IA or IB).

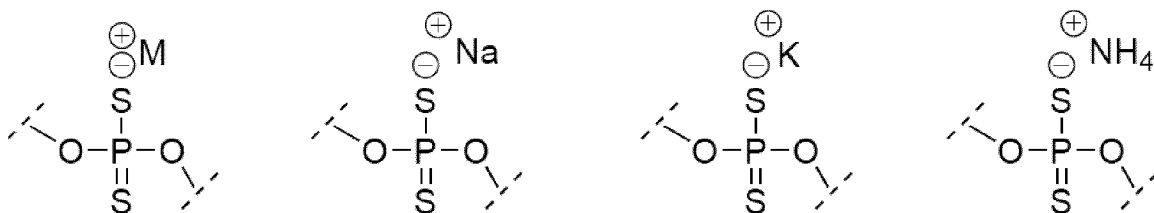
The invention also relates to a process for the manufacture of an oligonucleotide according to the invention and to a LNA nucleoside monomer useful in particular in the manufacture of on oligonucleotide according to the invention.

5 The invention also relates to a process for the manufacture of an oligonucleotide according to the invention and to a MOE nucleoside monomer useful in particular in the manufacture of on oligonucleotide according to the invention.

The invention further provides novel MOE and LNA monomers which may be used in the manufacture of on oligonucleotide according to the invention.

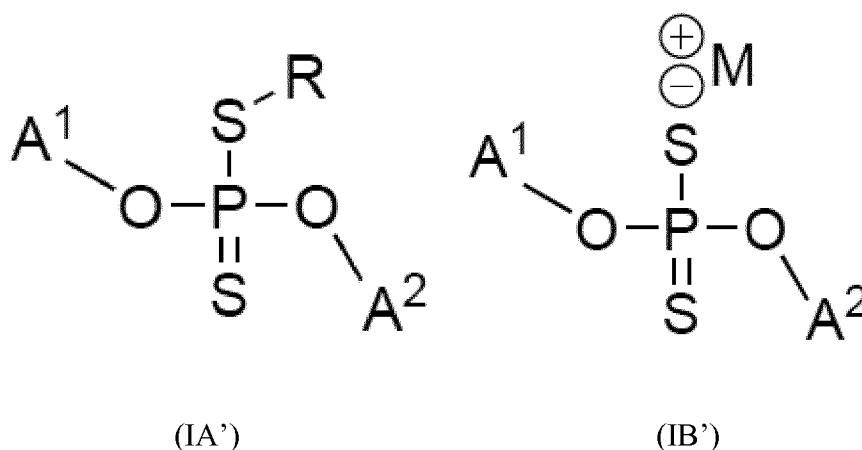
10 During oligonucleotide synthesis, the use of a protective R group is often used. After oligonucleotide synthesis, the protecting group is typically exchanged for either a hydrogen atom or cation like an alkali metal or an ammonium cation, such as when the oligonucleotide is in the form of a salt. The salt typically contains a cation, such as a metal cation, e.g. sodium or potassium cation or an ammonium cation. With regards antisense oligonucleotides, preferably R is hydrogen, or the the antisense oligonucleotide is in the
15 form of a salt (as shown in IB).

The phosphorodithioate internucleoside linkage of formula (IB) may, for example, be selected from the group consisting of:



20 wherein M+ is a cation, such as a metal cation, such as an alkali metal cation, such as a Na+ or K+ cation; or M+ is an ammonium cation. The oligonucleotide of the invention may therefore be in the form of an oligonucleotide salt, an alkali metal salt, such as a sodium salt, a potassium salt or an ammonium salt.

Alternatively represented, the oligonucleotide of the invention may comprise a phosphorodithioate internucleoside linkage of formula IA' or IB'



The invention further relates in particular to a gapmer oligonucleotide comprising a phosphorodithioate internucleoside linkage of formula (I), for formula IA or IB, or
 5 formula IA' or formula IB'.

The invention further relates in particular to a mixmer oligonucleotide comprising a phosphorodithioate internucleoside linkage of formula (I), for formula IA or IB, or
 formula IA' or formula IB'.

The invention further relates in particular to a totalmer oligonucleotide comprising a
 10 phosphorodithioate internucleoside linkage of formula (I), for formula IA or IB, or
 formula IA' or formula IB'.

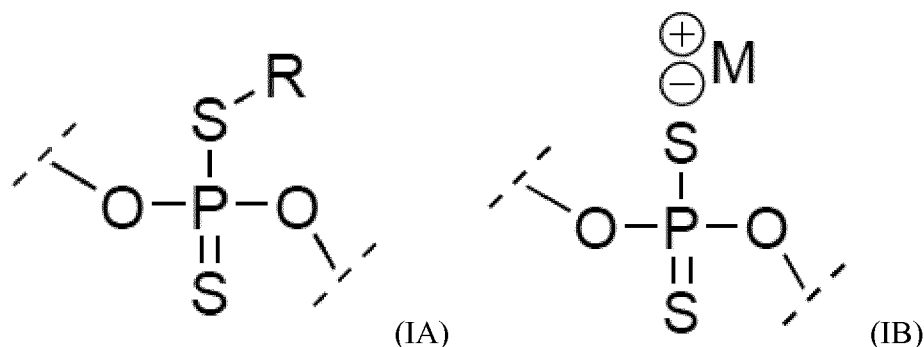
In preferred embodiments of the oligonucleotide of the invention at least one of the two nucleosides (A¹) and (A²) is a LNA nucleoside.

In preferred embodiments of the oligonucleotide of the invention at least one of the
 15 two nucleosides (A¹) and (A²) is a 2'-O-MOE nucleoside.

In preferred embodiments of the oligonucleotide of the invention, the oligonucleotide is a single stranded antisense oligonucleotide, at least one of the two nucleosides (A¹) and (A²) is a LNA nucleoside.

In preferred embodiments of the oligonucleotide of the invention the oligonucleotide
 20 is a single stranded antisense oligonucleotide, and at least one of the two nucleosides (A¹) and (A²) is a 2'-O-MOE nucleoside.

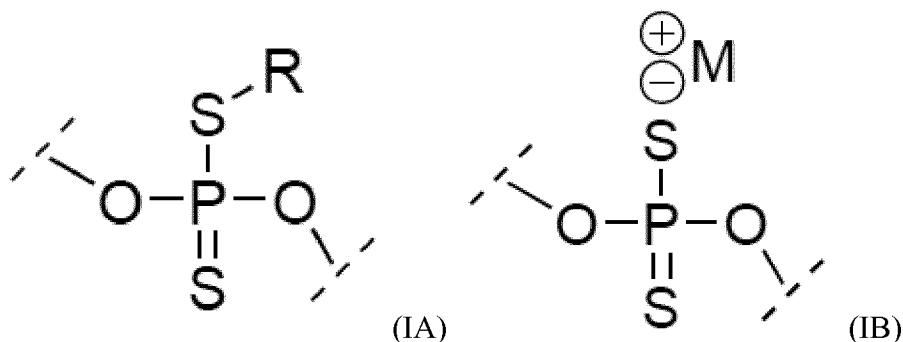
The invention provides an antisense oligonucleotide, for inhibition of a target RNA in a cell, wherein the antisense gapmer oligonucleotide comprises at least one phosphorodithioate internucleoside linkage of formula (IA) or (IB)



wherein in (IA) R is hydrogen or a phosphate protecting group, and in (IB) M⁺ is a cation, such as a metal cation, such as an alkali metal cation, such as a Na⁺ or K⁺ cation; or M⁺ is an ammonium cation, wherein the antisense oligonucleotide is or comprises an antisense
 5 gapmer oligonucleotide (referred to herein as a gapmer or a gapmer ligonucleotide),

The antisense oligonucleotide of the invention may therefore comprise or consist of a gapmer.

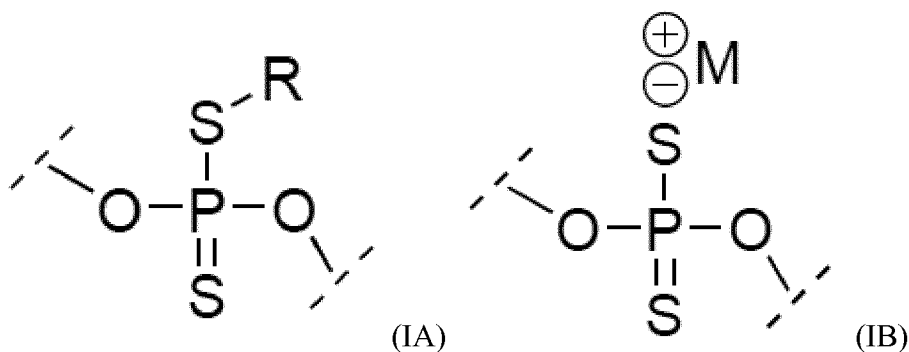
The invention provides for an antisense oligonucleotide comprising at least one phosphorodithioate internucleoside linkage formula IA or IB



10

wherein one of the two oxygen atoms is linked to the 3' carbon atom of an adjacent nucleoside (A¹) and the other one is linked to the 5' carbon atom of another adjacent nucleoside (A²), wherein at least one of the two nucleosides (A¹) and (A²) is a LNA nucleoside and wherein in (IA) R is hydrogen or a phosphate protecting group, and in
 15 (IB) M⁺ is a cation, such as a metal cation, such as an alkali metal cation, such as a Na⁺ or K⁺ cation; or M⁺ is an ammonium cation, wherein A² is the 3' terminal nucleoside of the oligonucleotide.

The invention provides for an antisense oligonucleotide comprising at least one phosphorodithioate internucleoside linkage of formula (IA or IB)

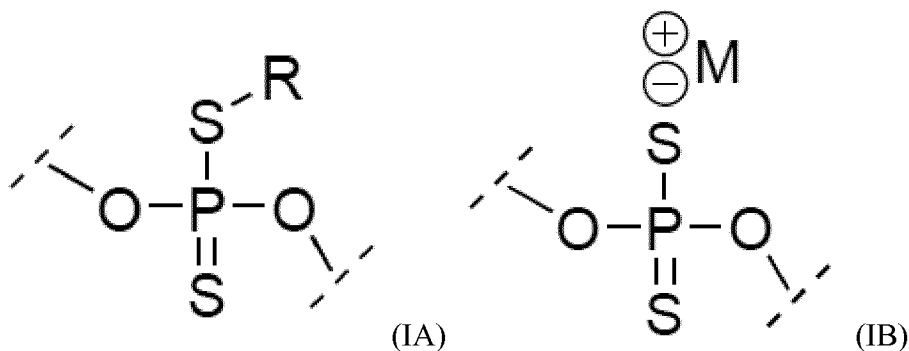


wherein one of the two oxygen atoms is linked to the 3' carbon atom of an adjacent nucleoside (A^1) and the other one is linked to the 5' carbon atom of another adjacent nucleoside (A^2), wherein at least one of the two nucleosides (A^1) and (A^2) is a LNA

5 nucleoside and wherein in (IA) R is hydrogen or a phosphate protecting group, and in (IB) M^+ is a cation, such as a metal cation, such as an alkali metal cation, such as a Na^+ or K^+ cation; or M^+ is an ammonium cation, wherein A^1 is the 5' terminal nucleoside of the oligonucleotide.

The invention provides for an antisense oligonucleotide comprising at least one

10 phosphorodithioate internucleoside linkage of formula (IA or IB)

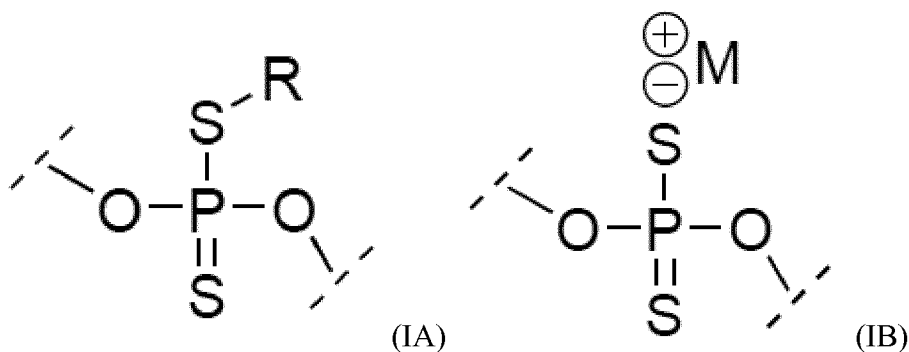


wherein one of the two oxygen atoms is linked to the 3' carbon atom of an adjacent nucleoside (A^1) and the other one is linked to the 5' carbon atom of another adjacent nucleoside (A^2), wherein at least one of the two nucleosides (A^1) and (A^2) is a 2-O-MOE

15 nucleoside and wherein in (IA) R is hydrogen or a phosphate protecting group, and in (IB) M^+ is a cation, such as a metal cation, such as an alkali metal cation, such as a Na^+ or K^+ cation; or M^+ is an ammonium cation, wherein A^2 is the 3' terminal nucleoside of the oligonucleotide.

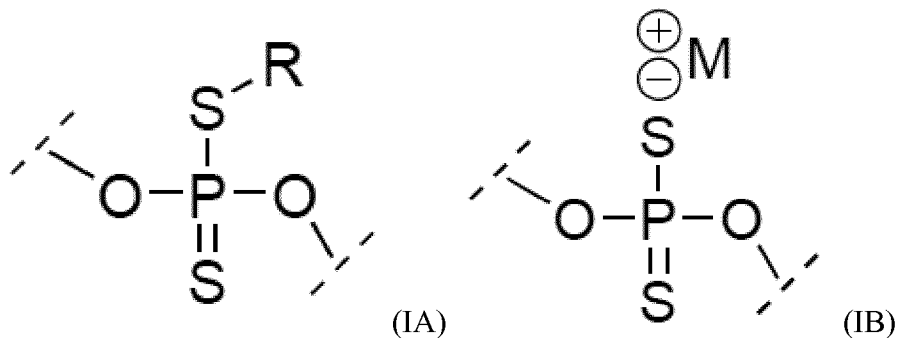
The invention provides for an antisense oligonucleotide comprising at least one

20 phosphorodithioate internucleoside linkage of formula (IA or IB)



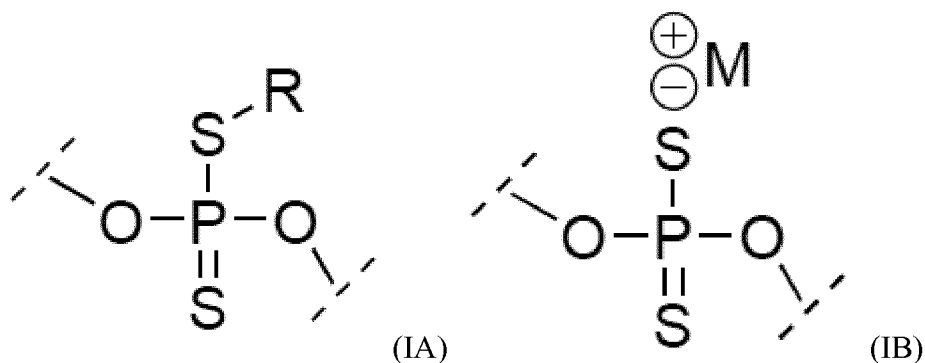
wherein one of the two oxygen atoms is linked to the 3' carbon atom of an adjacent nucleoside (A¹) and the other one is linked to the 5' carbon atom of another adjacent nucleoside (A²), wherein at least one of the two nucleosides (A¹) and (A²) is a 2-O-MOE
 5 nucleoside and wherein in (IA) R is hydrogen or a phosphate protecting group, and in (IB) M⁺ is a cation, such as a metal cation, such as an alkali metal cation, such as a Na⁺ or K⁺ cation; or M⁺ is an ammonium cation, wherein A¹ is the 5' terminal nucleoside of the oligonucleotide.

The invention provides for an antisense oligonucleotide comprising at least one
 10 phosphorodithioate internucleoside linkage of formula (IA or IB)



wherein one of the two oxygen atoms is linked to the 3' carbon atom of an adjacent nucleoside (A¹) and the other one is linked to the 5' carbon atom of another adjacent nucleoside (A²), wherein at least one of the two nucleosides (A¹) and (A²) is a 2' sugar
 15 modified nucleoside and wherein in (IA) R is hydrogen or a phosphate protecting group, and in (IB) M⁺ is a cation, such as a metal cation, such as an alkali metal cation, such as a Na⁺ or K⁺ cation; or M⁺ is an ammonium cation, and wherein A² is the 3' terminal nucleoside of the oligonucleotide.

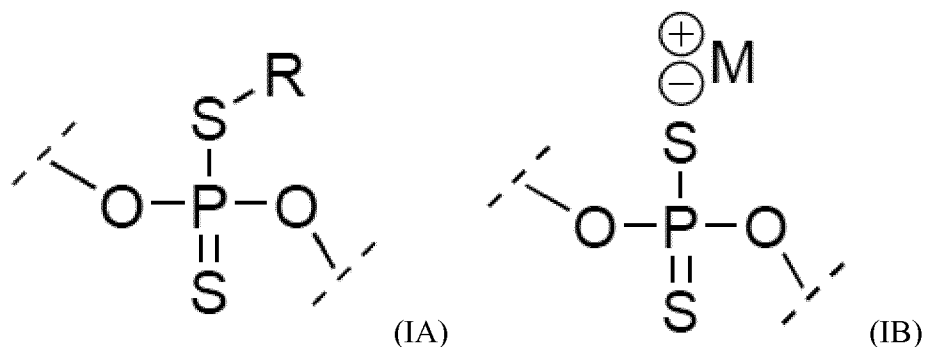
The invention provides for an antisense oligonucleotide comprising at least one
 20 phosphorodithioate internucleoside linkage of formula (IA or IB)



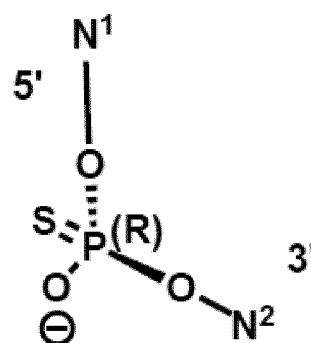
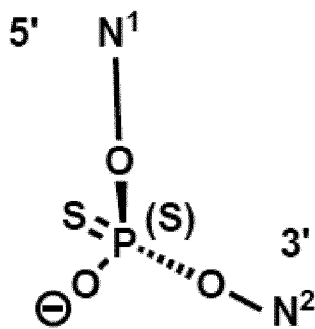
wherein one of the two oxygen atoms is linked to the 3' carbon atom of an adjacent nucleoside (A¹) and the other one is linked to the 5' carbon atom of another adjacent nucleoside (A²), wherein at least one of the two nucleosides (A¹) and (A²) is a 2' sugar modified nucleoside and wherein in (IA) R is hydrogen or a phosphate protecting group, and in (IB) M⁺ is a cation, such as a metal cation, such as an alkali metal cation, such as a Na⁺ or K⁺ cation; or M⁺ is an ammonium cation, and wherein A¹ is the 5' terminal nucleoside of the oligonucleotide.

The 2' sugar modified nucleoside may be independently selected from the group consisting of 2' sugar modified nucleoside selected from the group consisting of 2'-alkoxy-RNA, 2'-alkoxyalkoxy-RNA, 2'-amino-DNA, 2'-fluoro-RNA, 2'-fluoro-ANA and an LNA nucleoside.

The invention provides for a single stranded antisense oligonucleotide comprising at least one phosphorodithioate internucleoside linkage of formula (IA) or (IB)

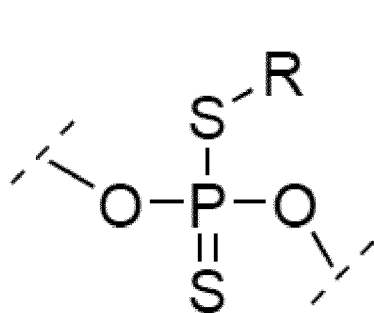


wherein one of the two oxygen atoms is linked to the 3' carbon atom of an adjacent nucleoside (A¹) and the other one is linked to the 5' carbon atom of another adjacent nucleoside (A²), and wherein in (IA) R is hydrogen or a phosphate protecting group, and in (IB) M⁺ is a cation, such as a metal cation, such as an alkali metal cation, such as a Na⁺ or K⁺ cation; or M⁺ is an ammonium cation, and wherein the single stranded oligonucleotide further comprises at least one stereodefined phosphorothioate internucleoside linkage, (Sp, S) or (Rp, R)

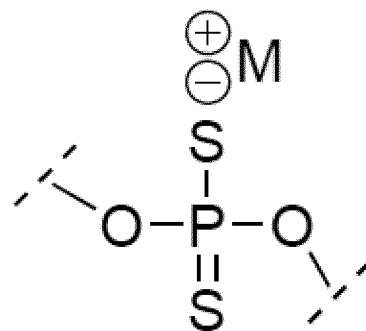


wherein N^1 and N^2 are nucleosides.

The invention also provides for a single stranded antisense oligonucleotide, for modulation of a RNA target in a cell, wherein the antisense oligonucleotide comprises or consists of a contiguous nucleotide sequence of 10 – 30 nucleotides in length, wherein the contiguous nucleotide sequence comprises one or more 2'sugar modified nucleosides, and wherein at least one of the internucleoside linkages present between the nucleosides of the contiguous nucleotide sequence is a phosphorodithioate linkage of formula IA or IB



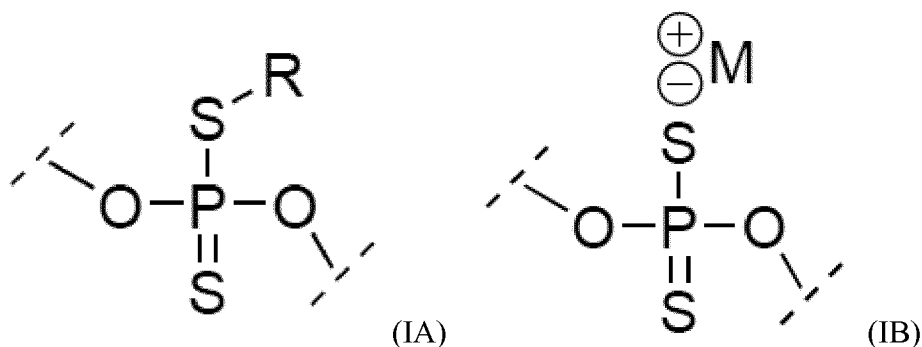
(IA)



(IB)

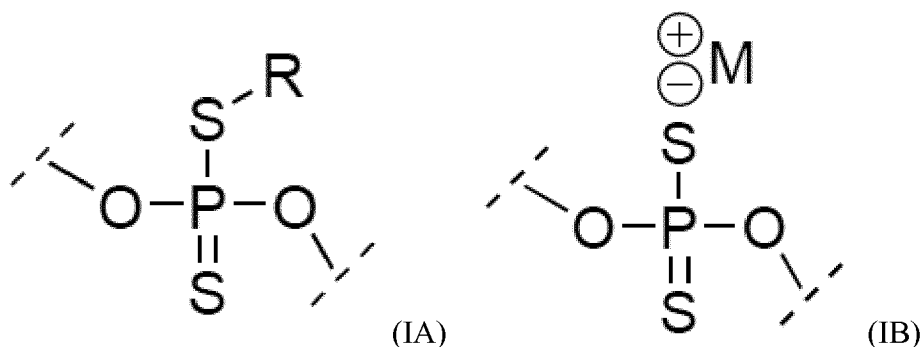
wherein one of the two oxygen atoms is linked to the 3'carbon atom of an adjacent nucleoside (A1) and the other one is linked to the 5'carbon atom of another adjacent nucleoside (A2) and wherein R is hydrogen or a phosphate protecting group.

The invention also provides for a single stranded antisense oligonucleotide, for modulation of a RNA target in a cell, wherein the antisense oligonucleotide comprises or consists of a contiguous nucleotide sequence of 10 – 30 nucleotides in length, wherein the contiguous nucleotide sequence comprises one or more 2'sugar modified nucleosides, and wherein at least one of the internucleoside linkages present between the nucleosides of the contiguous nucleotide sequence is a phosphorodithioate linkage of formula IA or IB



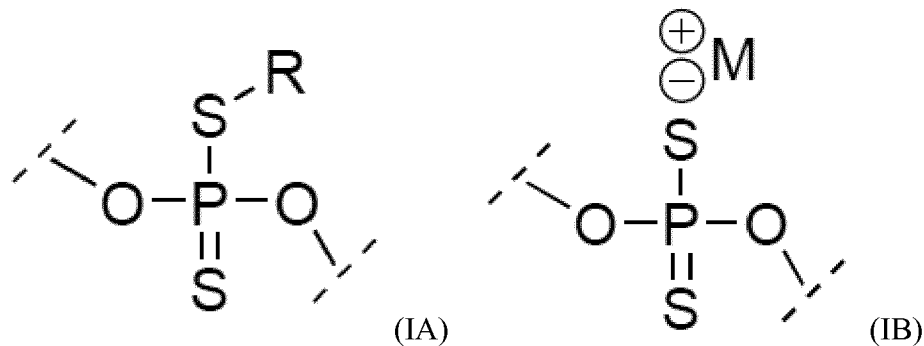
- wherein one of the two oxygen atoms is linked to the 3' carbon atom of an adjacent nucleoside (A1) and the other one is linked to the 5' carbon atom of another adjacent nucleoside (A2); and wherein in (IA) R is hydrogen or a phosphate protecting group, and
- 5 in (IB) M⁺ is a cation, such as a metal cation, such as an alkali metal cation, such as a Na⁺ or K⁺ cation; or M⁺ is an ammonium cation, and wherein the single stranded antisense oligonucleotide is for use in modulating the splicing of a pre-mRNA target RNA.

- The invention also provides for a single stranded antisense oligonucleotide, for modulation of a RNA target in a cell, wherein the antisense oligonucleotide comprises or
- 10 consists of a contiguous nucleotide sequence of 10 – 30 nucleotides in length, wherein the contiguous nucleotide sequence comprises one or more 2' sugar modified nucleosides, and wherein at least one of the internucleoside linkages present between the nucleosides of the contiguous nucleotide sequence is a phosphorodithioate linkage of formula IA or IB



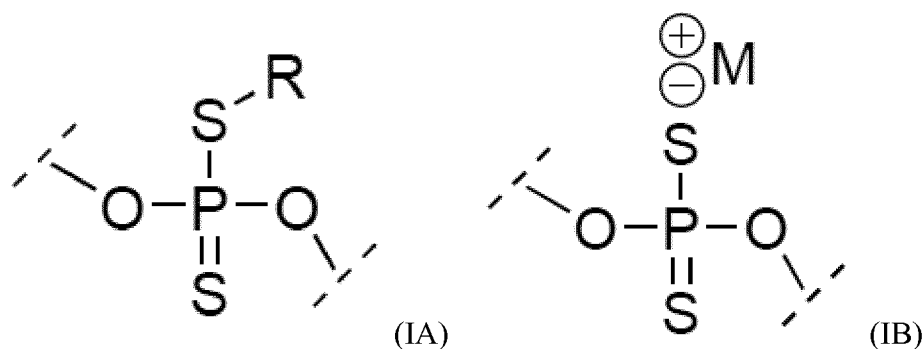
- 15 wherein one of the two oxygen atoms is linked to the 3' carbon atom of an adjacent nucleoside (A¹) and the other one is linked to the 5' carbon atom of another adjacent nucleoside (A²); and wherein in (IA) R is hydrogen or a phosphate protecting group, and in (IB) M⁺ is a cation, such as a metal cation, such as an alkali metal cation, such as a Na⁺ or K⁺ cation; or M⁺ is an ammonium cation, and wherein the single stranded antisense
- 20 oligonucleotide is for use in inhibiting the expression of a long-non coding RNA. See WO 2012/065143 for examples of lncRNAs which may be targeted by the compounds of the invention.

The invention also provides for a single stranded antisense oligonucleotide, for modulation of a RNA target in a cell, wherein the antisense oligonucleotide comprises or consists of a contiguous nucleotide sequence of 10 – 30 nucleotides in length, wherein the contiguous nucleotide sequence comprises one or more 2'sugar modified nucleosides, and
 5 wherein at least one of the internucleoside linkages present between the nucleosides of the contiguous nucleotide sequence is a phosphorodithioate linkage of formula IA or IB



wherein one of the two oxygen atoms is linked to the 3'carbon atom of an adjacent nucleoside (A¹) and the other one is linked to the 5'carbon atom of another adjacent
 10 nucleoside (A²); and wherein in (IA) R is hydrogen or a phosphate protecting group, and in (IB) M⁺ is a cation, such as a metal cation, such as an alkali metal cation, such as a Na⁺ or K⁺ cation; or M⁺ is an ammonium cation, and wherein the single stranded antisense oligonucleotide is for use in inhibiting the expression of a human mRNA or pre-mRNA target.

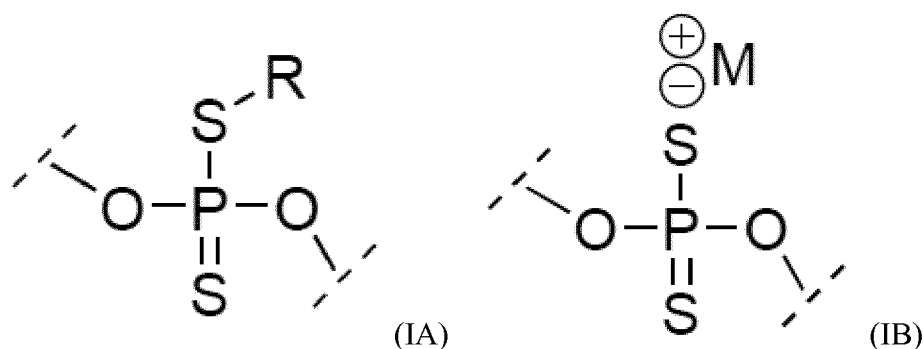
15 The invention also provides for a single stranded antisense oligonucleotide, for modulation of a RNA target in a cell, wherein the antisense oligonucleotide comprises or consists of a contiguous nucleotide sequence of 10 – 30 nucleotides in length, wherein the contiguous nucleotide sequence comprises one or more 2'sugar modified nucleosides, and wherein at least one of the internucleoside linkages present between the nucleosides of the
 20 contiguous nucleotide sequence is a phosphorodithioate linkage of formula IA or IB



wherein one of the two oxygen atoms is linked to the 3'carbon atom of an adjacent nucleoside (A¹) and the other one is linked to the 5'carbon atom of another adjacent nucleoside (A²); and wherein in (IA) R is hydrogen or a phosphate protecting group, and

in (IB) M^+ is a cation, such as a metal cation, such as an alkali metal cation, such as a Na^+ or K^+ cation; or M^+ is an ammonium cation, and wherein the single stranded antisense oligonucleotide is for use in inhibiting the expression of a viral RNA target. Suitable the viral RNA target may be HCV or HBV for example.

- 5 The invention also provides for a single stranded antisense oligonucleotide, for modulation of a RNA target in a cell, wherein the antisense oligonucleotide comprises or consists of a contiguous nucleotide sequence of 7 – 30 nucleotides in length, wherein the contiguous nucleotide sequence comprises one or more 2'sugar modified nucleosides, and wherein at least one of the internucleoside linkages present between the nucleosides of the
- 10 contiguous nucleotide sequence is a phosphorodithioate linkage of formula IA or IB



- wherein one of the two oxygen atoms is linked to the 3' carbon atom of an adjacent nucleoside (A^1) and the other one is linked to the 5' carbon atom of another adjacent nucleoside (A^2); and wherein in (IA) R is hydrogen or a phosphate protecting group, and
- 15 in (IB) M^+ is a cation, such as a metal cation, such as an alkali metal cation, such as a Na^+ or K^+ cation; or M^+ is an ammonium cation, and wherein the single stranded antisense oligonucleotide is for use in inhibiting the expression of a microRNA.

- For targeting a RNA target, e.g. a pre-mRNA target, an mRNA target, a viral RNA target, a microRNA or a long non coding RNA target, the oligonucleotide of the invention
- 20 is suitably capable of inhibiting the expression of the target RNA. This is achieved by the complementarity between the antisense oligonucleotide and the target RNA. Inhibition of the RNA target may be achieved by reducing the level of the RNA target or by blocking the function of the RNA target. RNA inhibition of an RNA target may suitably be achieved via recruitment of a cellular RNase such as RNaseH, e.g. via the use of a
- 25 gapmer, or may be achieved via a non nuclease mediated mechanism, such as a steric blocking mechanism (such as for microRNA inhibition, for splice modulating of pre-mRNAs, or for blocking the interaction between a long non coding RNA and chromatin).

- The invention also relates to a process for the manufacture of an oligonucleotide according to the invention and to a LNA or MOE nucleoside monomer useful in particular
- 30 in the manufacture of an oligonucleotide according to the invention.

The invention provides for a pharmaceutically acceptable salt of an oligonucleotide according to the invention, or a conjugate thereof, in particular a sodium or a potassium salt or an ammonium salt.

5 The invention provides for a conjugate comprising an oligonucleotide, or a pharmaceutically acceptable salt, thereof, and at least one conjugate moiety covalently attached to said oligonucleotide or said pharmaceutically acceptable salt, optionally via a linker moiety.

10 The invention provides for a pharmaceutical composition comprising an oligonucleotide, pharmaceutically acceptable salt or conjugate according to the invention and a therapeutically inert carrier.

The invention provides for an oligonucleotide, a pharmaceutically acceptable salt or a conjugate according to any the invention for use as a therapeutically active substance.

15 The invention provides for a method for the modulation of a target RNA in a cell which is expressing said RNA, said method comprising the step of administering an effective amount of the oligonucleotide, pharmaceutically acceptable salt, conjugate or composition according to the invention to the cell, wherein the oligonucleotide is complementary to the target RNA.

20 The invention provides for a method of modulation of a splicing of a target pre-RNA in a cell which is expressing said target pre-mRNA, said method comprising the step of administering an effective amount of the oligonucleotide, pharmaceutically acceptable salt, conjugate or composition according to the invention to the cell, wherein the oligonucleotide is complementary to the target RNA and is capable of modulating a splicing event in the pre-mRNA.

25 The invention provides for the use of an oligonucleotide, pharmaceutical salt, conjugate, or composition of the invention for inhibition of a pre-mRNA, an mRNA, or a long-non coding RNA in a cell, such as in a human cell.

The above methods or uses may be an in vitro method or an in vivo method.

The invention provides for the use of an oligonucleotide, pharmaceutical salt, conjugate, or composition of the invention in the manufacture of a medicament.

30 The invention provides for the use of a phosphorodithioate internucleoside linkage of formula IA or IB, for use for enhancing the in vitro or in vivo stability of a single stranded phosphorothioate antisense oligonucleotide.

The invention provides for the use of a phosphorodithioate internucleoside linkage of formula IA or IB, for use for enhancing the in vitro or in vivo duration of action a single stranded phosphorothioate antisense oligonucleotide.

5 The invention provides for the use of a phosphorodithioate internucleoside linkage of formula IA or IB, for use for enhancing cellular uptake or tissue distribution of a single stranded phosphorothioate antisense oligonucleotide.

The invention provides for the use of a phosphorodithioate internucleoside linkage of formula IA or IB, for use for enhancing uptake of a single stranded phosphorothioate antisense oligonucleotide into a tissue selected from the group consisting of skeletal
10 muscle, heart, epithelial cells, including retinal epithelial cells (e.g. for Htra1 targeting compounds), liver, kidney, or spleen.

For in vivo use a single stranded phosphorothioate antisense oligonucleotide may be a therapeutic oligonucleotide.

FIGURES

15 Figures 1-4 show the target mRNA levels in primary rat hepatocytes after 24 and 74 hours of administration of oligonucleotides according to the invention.

Figure 1 shows the target mRNA levels in primary rat hepatocytes after 24 and 74 hours of administration of oligonucleotide gapmers having a single phosphorodithioate internucleoside linkage according the invention in the gap.

20 Figure 2 shows the target mRNA levels in primary rat hepatocytes after 24 and 74 hours of administration of oligonucleotide gapmers having multiple phosphorodithioate internucleoside linkages according the invention in the gap.

Figure 3 shows the target mRNA levels in primary rat hepatocytes after 24 and 74 hours of administration of oligonucleotide gapmers having multiple phosphorodithioate
25 internucleoside linkages according the invention in the gap.

Figure 4 shows the target mRNA levels in primary rat hepatocytes after 24 and 74 hours of administration of oligonucleotide gapmers having phosphorodithioate internucleoside linkages according the invention in the flanks.

Figure 5 shows the thermal melting (T_m) of oligonucleotides containing a
30 phosphorodithioate internucleoside linkage according to the invention hybridized to RNA and DNA.

Figure 6 shows the stability of oligonucleotides containing a phosphorodithioate internucleoside linkage according to the invention in rat serum.

Figure 7: Exploring achiral phosphodithioate in the gap and flank regions of gapmers – residual mRNA levels after treatment of primary rat hepatocytes.

- 5 Figure 8: Exploring positional dependency and optimization of achiral phosphodithioate in the gap regions of gapmers – residual mRNA levels after treatment of primary rat hepatocytes.

Figures 9A-9B: Exploring achiral phosphodithioate in the gap regions of gapmers – effect on cellular uptake.

- 10 Figures 10A-10B: Introduction of achiral phosphorodithioate in the flank regions of gapmers provides increased potency, with a correlation between phosphorothioate load with increased potency (4 linkages > 3 linkages > 2 linkages > 1 linkage > no phosphorodithioate linkages in the flanks).

Figure 11: IC₅₀ values in difference cell types.

- 15 Figure 12: In vitro rat serum stability of 3' end protected LNA oligonucleotides.

Figure 13: In vivo evaluation of gapmers containing achiral phosphorodithioate linkages in the flanks and the gap regions – Target inhibition.

Figure 14A: In vivo evaluation of gapmers containing achiral phosphorodithioate linkages in the flanks and the gap regions – Tissue uptake.

- 20 Figure 14B: In vivo evaluation of gapmers containing achiral phosphorodithioate linkages in the flanks and the gap regions – Liver/kidney ratio.

Figures 15A and 15B: In vivo evaluation of gapmers containing achiral phosphorodithioate linkages in the flanks and the gap regions – metabolite analysis.

- 25 Figure 16: The prolonged duration of action with antisense oligonucleotides comprising achiral phosphorodithioate internucleoside linkages can be further enhanced by combination with stereodefined phosphorothioate internucleoside linkages.

Figure 17A: In vitro EC₅₀ determination of achiral phosphorodithioate gapmers targeting MALAT-1.

Figure 17B: In vivo potency of achiral phosphorodithioate gapmers targeting MALAT-1.

Figure 17C: In vivo study of achiral phosphorodithioate gapmers targeting MALAT-1 – tissue content

Figure 18A: In vitro study of achiral monophosphorothioate modified gapmer oligonucleotides targeting ApoB. Activity data.

- 5 Figure 18B: In vitro study of achiral monophosphorothioate modified gapmer oligonucleotides targeting ApoB. Cellular content data.

Figure 19A: In vitro study of chiral phosphorodithioate modified gapmer oligonucleotides targeting ApoB. Activity data.

- 10 Figure 19B: In vitro study of chiral phosphorodithioate modified gapmer oligonucleotides targeting ApoB. Cellular content data.

- Figure 20: Effects of achiral phosphorodithioates (P2S) internucleoside linkages present in splice-switching oligonucleotide targeting the 3' splice site of TNFRSF1B. Human Colo 205 cells was seeded in a 96 well plate and subjected to 5 μ M (A) and 25 μ M (B) of oligo, respectively. The percentage of exon 7 skipping was analyzed by droplet digital PCR
- 15 using probes targeting the exon 6-8 junction and compared to the total amount of TNFRSF1B by the assay targeting exon 2-3. SSO#26 is the parent oligo, and SSO#27 is a negative control not targeting TNFRSF1B.

- Figure 21: Stability assay using S1 nuclease. Dithioate containing oligos were incubated with S1 nuclease for 30 and 120 minutes, respectively. The oligos were visualized on a
- 20 15% TBE-Urea gel. As marker of the migration of intact oligos (SSO#14) was included without being subjected to S1 nuclease.

DEFINITIONS

- In the present description the term “alkyl”, alone or in combination, signifies a straight-chain or branched-chain alkyl group with 1 to 8 carbon atoms, particularly a
- 25 straight or branched-chain alkyl group with 1 to 6 carbon atoms and more particularly a straight or branched-chain alkyl group with 1 to 4 carbon atoms. Examples of straight-chain and branched-chain C₁-C₈ alkyl groups are methyl, ethyl, propyl, isopropyl, butyl, isobutyl, tert.-butyl, the isomeric pentyls, the isomeric hexyls, the isomeric heptyls and the isomeric octyls, particularly methyl, ethyl, propyl, butyl and pentyl. Particular examples of
- 30 alkyl are methyl, ethyl and propyl.

The term “cycloalkyl”, alone or in combination, signifies a cycloalkyl ring with 3 to 8 carbon atoms and particularly a cycloalkyl ring with 3 to 6 carbon atoms. Examples of cycloalkyl are cyclopropyl, cyclobutyl, cyclopentyl, cyclohexyl, cycloheptyl and

cyclooctyl, more particularly cyclopropyl and cyclobutyl. A particular example of “cycloalkyl” is cyclopropyl.

The term “alkoxy”, alone or in combination, signifies a group of the formula alkyl-O- in which the term “alkyl” has the previously given significance, such as methoxy, ethoxy, n-propoxy, isopropoxy, n-butoxy, isobutoxy, sec.butoxy and tert.butoxy. Particular “alkoxy” are methoxy and ethoxy. Methoxyethoxy is a particular example of “alkoxyalkoxy”.

The term “oxy”, alone or in combination, signifies the -O- group.

The term “alkenyl”, alone or in combination, signifies a straight-chain or branched hydrocarbon residue comprising an olefinic bond and up to 8, preferably up to 6, particularly preferred up to 4 carbon atoms. Examples of alkenyl groups are ethenyl, 1-propenyl, 2-propenyl, isopropenyl, 1-butenyl, 2-butenyl, 3-butenyl and isobutenyl.

The term “alkynyl”, alone or in combination, signifies a straight-chain or branched hydrocarbon residue comprising a triple bond and up to 8, particularly 2 carbon atoms.

The terms “halogen” or “halo”, alone or in combination, signifies fluorine, chlorine, bromine or iodine and particularly fluorine, chlorine or bromine, more particularly fluorine. The term “halo”, in combination with another group, denotes the substitution of said group with at least one halogen, particularly substituted with one to five halogens, particularly one to four halogens, i.e. one, two, three or four halogens.

The term “haloalkyl”, alone or in combination, denotes an alkyl group substituted with at least one halogen, particularly substituted with one to five halogens, particularly one to three halogens. Examples of haloalkyl include monofluoro-, difluoro- or trifluoromethyl, -ethyl or -propyl, for example 3,3,3-trifluoropropyl, 2-fluoroethyl, 2,2,2-trifluoroethyl, fluoromethyl or trifluoromethyl. Fluoromethyl, difluoromethyl and trifluoromethyl are particular “haloalkyl”.

The term “halocycloalkyl”, alone or in combination, denotes a cycloalkyl group as defined above substituted with at least one halogen, particularly substituted with one to five halogens, particularly one to three halogens. Particular example of “halocycloalkyl” are halocyclopropyl, in particular fluorocyclopropyl, difluorocyclopropyl and trifluorocyclopropyl.

The terms “hydroxyl” and “hydroxy”, alone or in combination, signify the -OH group.

The terms “thiohydroxyl” and “thiohydroxy”, alone or in combination, signify the -SH group.

The term “carbonyl”, alone or in combination, signifies the -C(O)- group.

5 The term “carboxy” or “carboxyl”, alone or in combination, signifies the -COOH group.

The term “amino”, alone or in combination, signifies the primary amino group (-NH₂), the secondary amino group (-NH-), or the tertiary amino group (-N-).

The term “alkylamino”, alone or in combination, signifies an amino group as defined above substituted with one or two alkyl groups as defined above.

10 The term “sulfonyl”, alone or in combination, means the -SO₂ group.

The term “sulfinyl”, alone or in combination, signifies the -SO- group.

The term “sulfanyl”, alone or in combination, signifies the -S- group.

The term “cyano”, alone or in combination, signifies the -CN group.

The term “azido”, alone or in combination, signifies the -N₃ group.

15 The term “nitro”, alone or in combination, signifies the NO₂ group.

The term “formyl”, alone or in combination, signifies the -C(O)H group.

The term “carbamoyl”, alone or in combination, signifies the -C(O)NH₂ group.

The term “cabamido”, alone or in combination, signifies the -NH-C(O)-NH₂ group.

20 The term “aryl”, alone or in combination, denotes a monovalent aromatic carbocyclic mono- or bicyclic ring system comprising 6 to 10 carbon ring atoms, optionally substituted with 1 to 3 substituents independently selected from halogen, hydroxyl, alkyl, alkenyl, alkynyl, alkoxy, alkoxyalkyl, alkenyloxy, carboxyl, alkoxycarbonyl, alkylcarbonyl and formyl. Examples of aryl include phenyl and naphthyl, in particular phenyl.

25 The term “heteroaryl”, alone or in combination, denotes a monovalent aromatic heterocyclic mono- or bicyclic ring system of 5 to 12 ring atoms, comprising 1, 2, 3 or 4 heteroatoms selected from N, O and S, the remaining ring atoms being carbon, optionally substituted with 1 to 3 substituents independently selected from halogen, hydroxyl, alkyl, alkenyl, alkynyl, alkoxy, alkoxyalkyl, alkenyloxy, carboxyl, alkoxycarbonyl,

alkylcarbonyl and formyl. Examples of heteroaryl include pyrrolyl, furanyl, thienyl, imidazolyl, oxazolyl, thiazolyl, triazolyl, oxadiazolyl, thiadiazolyl, tetrazolyl, pyridinyl, pyrazinyl, pyrazolyl, pyridazinyl, pyrimidinyl, triazinyl, azepinyl, diazepinyl, isoxazolyl, benzofuranyl, isothiazolyl, benzothienyl, indolyl, isoindolyl, isobenzofuranyl, 5 benzimidazolyl, benzoxazolyl, benzoisoxazolyl, benzothiazolyl, benzoisothiazolyl, benzooxadiazolyl, benzothiadiazolyl, benzotriazolyl, purinyl, quinoliny, isoquinoliny, quinazolinyl, quinoxaliny, carbazolyl or acridinyl.

The term “heterocyclyl”, alone or in combination, signifies a monovalent saturated or partly unsaturated mono- or bicyclic ring system of 4 to 12, in particular 4 to 9 ring 10 atoms, comprising 1, 2, 3 or 4 ring heteroatoms selected from N, O and S, the remaining ring atoms being carbon, optionally substituted with 1 to 3 substituents independently selected from halogen, hydroxyl, alkyl, alkenyl, alkynyl, alkoxy, alkoxyalkyl, alkenyloxy, carboxyl, alkoxycarbonyl, alkylcarbonyl and formyl. Examples for monocyclic saturated heterocyclyl are azetidiny, pyrrolidiny, tetrahydrofuranyl, tetrahydro-thienyl, 15 pyrazolidiny, imidazolidiny, oxazolidiny, isoxazolidiny, thiazolidiny, piperidiny, tetrahydropyranyl, tetrahydrothiopyranyl, piperazinyl, morpholiny, thiomorpholiny, 1,1-dioxo-thiomorpholin-4-yl, azepanyl, diazepanyl, homopiperazinyl, or oxazepanyl. Examples for bicyclic saturated heterocycloalkyl are 8-aza-bicyclo[3.2.1]octyl, quinuclidiny, 8-oxa-3-aza-bicyclo[3.2.1]octyl, 9-aza-bicyclo[3.3.1]nonyl, 3-oxa-9-aza-bicyclo[3.3.1]nonyl, or 3-thia-9-aza-bicyclo[3.3.1]nonyl. Examples for partly unsaturated heterocycloalkyl are dihydrofuryl, imidazoliny, dihydro-oxazolyl, tetrahydro-pyridiny or dihydropyranyl.

The term “pharmaceutically acceptable salts” refers to those salts which retain the biological effectiveness and properties of the free bases or free acids, which are not 25 biologically or otherwise undesirable. The salts are formed with inorganic acids such as hydrochloric acid, hydrobromic acid, sulfuric acid, nitric acid, phosphoric acid, particularly hydrochloric acid, and organic acids such as acetic acid, propionic acid, glycolic acid, pyruvic acid, oxalic acid, maleic acid, malonic acid, succinic acid, fumaric acid, tartaric acid, citric acid, benzoic acid, cinnamic acid, mandelic acid, methanesulfonic acid, ethanesulfonic acid, p-toluenesulfonic acid, salicylic acid, N-acetylcystein. In 30 addition, these salts may be prepared from addition of an inorganic base or an organic base to the free acid. Salts derived from an inorganic base include, but are not limited to, the sodium, potassium, lithium, ammonium, calcium, magnesium salts. Salts derived from organic bases include, but are not limited to salts of primary, secondary, and tertiary amines, substituted amines including naturally occurring substituted amines, cyclic amines and basic ion exchange resins, such as isopropylamine, trimethylamine, diethylamine, triethylamine, tripropylamine, ethanolamine, lysine, arginine, N-ethylpiperidine, 35 piperidine, polyamine resins. The oligonucleotide of the invention can also be present in

the form of zwitterions. Particularly preferred pharmaceutically acceptable salts of the invention are the sodium, lithium, potassium and trialkylammonium salts.

The term “protecting group”, alone or in combination, signifies a group which selectively blocks a reactive site in a multifunctional compound such that a chemical
5 reaction can be carried out selectively at another unprotected reactive site. Protecting groups can be removed. Exemplary protecting groups are amino-protecting groups, carboxy-protecting groups or hydroxy-protecting groups.

“Phosphate protecting group” is a protecting group of the phosphate group. Examples of phosphate protecting group are 2-cyanoethyl and methyl. A particular
10 example of phosphate protecting group is 2-cyanoethyl.

“Hydroxyl protecting group” is a protecting group of the hydroxyl group and is also used to protect thiol groups. Examples of hydroxyl protecting groups are acetyl (Ac), benzoyl (Bz), benzyl (Bn), β -methoxyethoxymethyl ether (MEM), dimethoxytrityl (or bis-(4-methoxyphenyl)phenylmethyl) (DMT), trimethoxytrityl (or tris-(4-
15 methoxyphenyl)phenylmethyl) (TMT), methoxymethyl ether (MOM), methoxytrityl [(4-methoxyphenyl)diphenylmethyl (MMT), p-methoxybenzyl ether (PMB), methylthiomethyl ether, pivaloyl (Piv), tetrahydropyranyl (THP), tetrahydrofuran (THF), trityl or triphenylmethyl (Tr), silyl ether (for example trimethylsilyl (TMS), tert-butyl dimethylsilyl (TBDMS), tri-iso-propylsilyloxymethyl (TOM) and triisopropylsilyl
20 (TIPS) ethers), methyl ethers and ethoxyethyl ethers (EE). Particular examples of hydroxyl protecting group are DMT and TMT, in particular DMT.

“Thiohydroxyl protecting group” is a protecting group of the thiohydroxyl group. Examples of thiohydroxyl protecting groups are those of the “hydroxyl protecting group”.

If one of the starting materials or compounds of the invention contain one or more
25 functional groups which are not stable or are reactive under the reaction conditions of one or more reaction steps, appropriate protecting groups (as described *e.g.* in “Protective Groups in Organic Chemistry” by T. W. Greene and P. G. M. Wuts, 3rd Ed., 1999, Wiley, New York) can be introduced before the critical step applying methods well known in the art. Such protecting groups can be removed at a later stage of the synthesis using standard
30 methods described in the literature. Examples of protecting groups are tert-butoxycarbonyl (Boc), 9-fluorenylmethyl carbamate (Fmoc), 2-trimethylsilylethyl carbamate (Teoc), carbobenzyloxy (Cbz) and p-methoxybenzyloxycarbonyl (Moz).

The compounds described herein can contain several asymmetric centers and can be present in the form of optically pure enantiomers, mixtures of enantiomers such as, for

example, racemates, mixtures of diastereoisomers, diastereoisomeric racemates or mixtures of diastereoisomeric racemates.

Oligonucleotide

The term “oligonucleotide” as used herein is defined as it is generally understood by the skilled person as a molecule comprising two or more covalently linked nucleosides. Such covalently bound nucleosides may also be referred to as nucleic acid molecules or oligomers. Oligonucleotides are commonly made in the laboratory by solid-phase chemical synthesis followed by purification. When referring to a sequence of the oligonucleotide, reference is made to the sequence or order of nucleobase moieties, or modifications thereof, of the covalently linked nucleotides or nucleosides. The oligonucleotide of the invention is man-made, and is chemically synthesized, and is typically purified or isolated. The oligonucleotide of the invention may comprise one or more modified nucleosides or nucleotides.

Antisense oligonucleotides

The term “Antisense oligonucleotide” as used herein is defined as oligonucleotides capable of modulating expression of a target gene by hybridizing to a target nucleic acid, in particular to a contiguous sequence on a target nucleic acid. The antisense oligonucleotides are not essentially double stranded and are therefore not siRNAs or shRNAs. Preferably, the antisense oligonucleotides of the present invention are single stranded. It is understood that single stranded oligonucleotides of the present invention can form hairpins or intermolecular duplex structures (duplex between two molecules of the same oligonucleotide), as long as the degree of intra or inter self complementarity is less than 50% across of the full length of the oligonucleotide.

Modulation of expression

The term “modulation of expression” as used herein is to be understood as an overall term for an oligonucleotide’s ability to alter the expression of or alter the level of the target nucleic acid. Modulation of expression may be determined by comparison to expression or level of the target nucleic acid prior to administration of the oligonucleotide, or modulation of expression may be determined by reference to a control experiment where the oligonucleotide of the invention is not administered. It is generally understood that the control is an individual or target cell treated with a saline composition or an individual or target cell treated with a non-targeting oligonucleotide (mock).

One type of modulation is the ability of an oligonucleotide’s ability to inhibit, down-regulate, reduce, suppress, remove, stop, block, prevent, lessen, lower, avoid or terminate expression of the target nucleic acid e.g. by degradation of the target nucleic acid (e.g. via

RNaseH1 mediated degradation) or blockage of transcription. Another type of modulation is an oligonucleotide's ability to restore, increase or enhance expression of the target RNA, e.g. modulating the splicing event on a target pre-mRNA, or via blockage of inhibitory mechanisms such as microRNA repression of an mRNA.

5 ***Contiguous Nucleotide Sequence***

The term "contiguous nucleotide sequence" refers to the region of the oligonucleotide which is complementary to, such as fully complementary to, the target nucleic acid. The term is used interchangeably herein with the term "contiguous nucleobase sequence" and the term "oligonucleotide motif sequence". In some
10 embodiments all the nucleotides of the oligonucleotide constitute the contiguous nucleotide sequence. In some embodiments the oligonucleotide comprises the contiguous nucleotide sequence, such as a F-G-F' gapmer region, and may optionally comprise further nucleotide(s), for example a nucleotide linker region which may be used to attach a functional group to the contiguous nucleotide sequence, e.g. region D or D'. The
15 nucleotide linker region may or may not be complementary to the target nucleic acid. The antisense oligonucleotide mixmer referred to herein may comprise or may consist of the contiguous nucleotide sequence.

Nucleotides

Nucleotides are the building blocks of oligonucleotides and polynucleotides, and for
20 the purposes of the present invention include both naturally occurring and non-naturally occurring nucleotides. In nature, nucleotides, such as DNA and RNA nucleotides comprise a ribose sugar moiety, a nucleobase moiety and one or more phosphate groups (which is absent in nucleosides). Nucleosides and nucleotides may also interchangeably be referred to as "units" or "monomers".

25 ***Modified nucleoside***

The term "modified nucleoside" or "nucleoside modification" as used herein refers to nucleosides modified as compared to the equivalent DNA or RNA nucleoside by the introduction of one or more modifications of the sugar moiety or the (nucleo)base moiety. In a preferred embodiment the modified nucleoside comprises a modified sugar moiety.
30 The term modified nucleoside may also be used herein interchangeably with the term "nucleoside analogue" or modified "units" or modified "monomers". Nucleosides with an unmodified DNA or RNA sugar moiety are termed DNA or RNA nucleosides herein. Nucleosides with modifications in the base region of the DNA or RNA nucleoside are still generally termed DNA or RNA if they allow Watson Crick base pairing.

35 ***Modified internucleoside linkage***

The term “modified internucleoside linkage” is defined as generally understood by the skilled person as linkages other than phosphodiester (PO) linkages, that covalently couples two nucleosides together. The oligonucleotides of the invention may therefore comprise modified internucleoside linkages. In some embodiments, the modified
5 internucleoside linkage increases the nuclease resistance of the oligonucleotide compared to a phosphodiester linkage. For naturally occurring oligonucleotides, the internucleoside linkage includes phosphate groups creating a phosphodiester bond between adjacent nucleosides. Modified internucleoside linkages are particularly useful in stabilizing oligonucleotides for *in vivo* use, and may serve to protect against nuclease cleavage at
10 regions of DNA or RNA nucleosides in the oligonucleotide of the invention, for example within the gap region of a gapmer oligonucleotide, as well as in regions of modified nucleosides, such as region F and F’.

In an embodiment, the oligonucleotide comprises one or more internucleoside linkages modified from the natural phosphodiester, such one or more modified
15 internucleoside linkages that is for example more resistant to nuclease attack. Nuclease resistance may be determined by incubating the oligonucleotide in blood serum or by using a nuclease resistance assay (e.g. snake venom phosphodiesterase (SVPD)), both are well known in the art. Internucleoside linkages which are capable of enhancing the nuclease resistance of an oligonucleotide are referred to as nuclease resistant
20 internucleoside linkages. In some embodiments at least 50% of the internucleoside linkages in the oligonucleotide, or contiguous nucleotide sequence thereof, are modified, such as at least 60%, such as at least 70%, such as at least 80 or such as at least 90% of the internucleoside linkages in the oligonucleotide, or contiguous nucleotide sequence thereof, are nuclease resistant internucleoside linkages. In some embodiments all of the
25 internucleoside linkages of the oligonucleotide, or contiguous nucleotide sequence thereof, are nuclease resistant internucleoside linkages. It will be recognized that, in some embodiments the nucleosides which link the oligonucleotide of the invention to a non-nucleotide functional group, such as a conjugate, may be phosphodiester.

A preferred modified internucleoside linkage for use in the oligonucleotide of the
30 invention is phosphorothioate.

Phosphorothioate internucleoside linkages are particularly useful due to nuclease resistance, beneficial pharmacokinetics and ease of manufacture. In some embodiments at least 50% of the internucleoside linkages in the oligonucleotide, or contiguous nucleotide sequence thereof, are phosphorothioate, such as at least 60%, such as at least 70%, such as
35 at least 80% or such as at least 90% of the internucleoside linkages in the oligonucleotide, or contiguous nucleotide sequence thereof, are phosphorothioate. In some embodiments, other than the phosphorodithioate internucleoside linkages, all of the internucleoside

linkages of the oligonucleotide, or contiguous nucleotide sequence thereof, are phosphorothioate. In some embodiments, the oligonucleotide of the invention comprises both phosphorothioate internucleoside linkages and at least one phosphodiester linkage, such as 2, 3 or 4 phosphodiester linkages, in addition to the phosphorodithioate linkage(s).

- 5 In a gapmer oligonucleotide, phosphodiester linkages, when present, are suitably not located between contiguous DNA nucleosides in the gap region G.

Nuclease resistant linkages, such as phosphorothioate linkages, are particularly useful in oligonucleotide regions capable of recruiting nuclease when forming a duplex with the target nucleic acid, such as region G for gapmers. Phosphorothioate linkages may, however, also be useful in non-nuclease recruiting regions and/or affinity enhancing regions such as regions F and F' for gapmers. Gapmer oligonucleotides may, in some
10 embodiments comprise one or more phosphodiester linkages in region F or F', or both region F and F', which the internucleoside linkage in region G may be fully phosphorothioate.

- 15 Advantageously, all the internucleoside linkages in the contiguous nucleotide sequence of the oligonucleotide, or all the internucleoside linkages of the oligonucleotide, are phosphorothioate linkages.

It is recognized that, as disclosed in EP 2 742 135, antisense oligonucleotides may comprise other internucleoside linkages (other than phosphodiester and phosphorothioate),
20 for example alkyl phosphonate/methyl phosphonate internucleosides, which according to EP 2 742 135 may for example be tolerated in an otherwise DNA phosphorothioate the gap region.

Stereorandom Phosphorothioate Linkages

Phosphorothioate linkages are internucleoside phosphate linkages where one of the
25 non-bridging oxygens has been substituted with a sulfur. The substitution of one of the non-bridging oxygens with a sulfur introduces a chiral center, and as such within a single phosphorothioate oligonucleotide, each phosphorothioate internucleoside linkage will be either in the S (Sp) or R (Rp) stereoisomers. Such internucleoside linkages are referred to as "chiral internucleoside linkages". By comparison, phosphodiester internucleoside
30 linkages are non-chiral as they have two non-terminal oxygen atoms.

The designation of the chirality of a stereocenter is determined by standard Cahn-Ingold-Prelog rules (CIP priority rules) first published in Cahn, R.S.; Ingold, C.K.; Prelog, V. (1966) "Specification of Molecular Chirality" *Angewandte Chemie International Edition* 5 (4): 385–415. doi:10.1002/anie.196603851.

During standard oligonucleotide synthesis the stereoselectivity of the coupling and the following sulfurization is not controlled. For this reason, the stereochemistry of each phosphorothioate internucleoside linkages is randomly Sp or Rp, and as such a phosphorothioate oligonucleotide produced by traditional oligonucleotide synthesis

5 actually can exist in as many as 2^X different phosphorothioate diastereoisomers, where X is the number of phosphorothioate internucleoside linkages. Such oligonucleotides are referred to as stereorandom phosphorothioate oligonucleotides herein, and do not contain any stereodefined internucleoside linkages. Stereorandom phosphorothioate oligonucleotides are therefore mixtures of individual diastereoisomers originating from the

10 non-stereodefined synthesis. In this context the mixture is defined as up to 2^X different phosphorothioate diastereoisomers.

Stereodefined Internucleoside Linkages

A stereodefined internucleoside linkage is a chiral internucleoside linkage having a diastereoisomeric excess for one of its two diastereomeric forms, Rp or Sp.

15 It should be recognized that stereoselective oligonucleotide synthesis methods used in the art typically provide at least about 90% or at least about 95% diastereoselectivity at each chiral internucleoside linkage, and as such up to about 10%, such as about 5% of oligonucleotide molecules may have the alternative diastereoisomeric form.

In some embodiments the diastereoisomeric ratio of each stereodefined chiral internucleoside linkage is at least about 90:10. In some embodiments the diastereoisomeric ratio of each chiral internucleoside linkage is at least about 95:5.

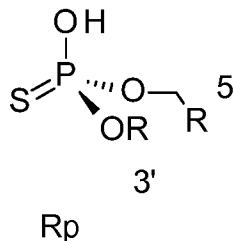
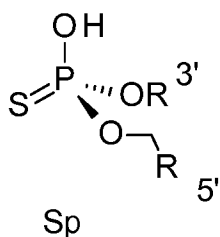
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The stereodefined phosphorothioate linkage is a particular example of stereodefined internucleoside linkage.

Stereodefined phosphorothioate linkage

25 A stereodefined phosphorothioate linkage is a phosphorothioate linkage having a diastereomeric excess for one of its two diastereoisomeric forms, Rp or Sp.

The Rp and Sp configurations of the phosphorothioate internucleoside linkages are presented below



Where the 3' R group represents the 3' position of the adjacent nucleoside (a 5' nucleoside), and the 5' R group represents the 5' position of the adjacent nucleoside (a 3' nucleoside).

Rp internucleoside linkages may also be represented as srP, and Sp internucleoside
5 linkages may be represented as ssP herein.

In a particular embodiment, the diastereomeric ratio of each stereodefined phosphorothioate linkage is at least about 90:10 or at least 95:5.

In some embodiments the diastereomeric ratio of each stereodefined phosphorothioate linkage is at least about 97:3. In some embodiments the diastereomeric
10 ratio of each stereodefined phosphorothioate linkage is at least about 98:2. In some embodiments the diastereomeric ratio of each stereodefined phosphorothioate linkage is at least about 99:1.

In some embodiments a stereodefined internucleoside linkage is in the same diastereomeric form (Rp or Sp) in at least 97%, such as at least 98%, such as at least 99%,
15 or (essentially) all of the oligonucleotide molecules present in a population of the oligonucleotide molecule.

Diastereomeric purity can be measured in a model system only having an achiral backbone (*i.e.* phosphodiester). It is possible to measure the diastereomeric purity of each monomer by *e.g.* coupling a monomer having a stereodefined internucleoside linkage to the
20 following model-system "5' t-po-t-po-t-po 3'". The result of this will then give : 5' DMTr-t-srp-t-po-t-po-t-po 3' or 5' DMTr-t-ssp-t-po-t-po-t-po 3' which can be separated using HPLC. The diastereomeric purity is determined by integrating the UV signal from the two possible diastereoisomers and giving a ratio of these *e.g.* 98:2, 99:1 or >99:1.

It will be understood that the diastereomeric purity of a specific single
25 diastereoisomer (a single stereodefined oligonucleotide molecule) will be a function of the coupling selectivity for the defined stereocenter at each internucleoside position, and the number of stereodefined internucleoside linkages to be introduced. By way of example, if the coupling selectivity at each position is 97%, the resulting purity of the stereodefined oligonucleotide with 15 stereodefined internucleoside linkages will be 0.97^{15} , *i.e.* 63% of
30 the desired diastereoisomer as compared to 37% of the other diastereoisomers. The purity of the defined diastereoisomer may after synthesis be improved by purification, for example by HPLC, such as ion exchange chromatography or reverse phase chromatography.

In some embodiments, a stereodefined oligonucleotide refers to a population of an oligonucleotide wherein at least about 40%, such as at least about 50% of the population is of the desired diastereoisomer.

Alternatively stated, in some embodiments, a stereodefined oligonucleotide refers to a population of oligonucleotides wherein at least about 40%, such as at least about 50%, of the population consists of the desired (specific) stereodefined internucleoside linkage motifs (also termed stereodefined motif).

For stereodefined oligonucleotides which comprise both stereorandom and stereodefined internucleoside chiral centers, the purity of the stereodefined oligonucleotide is determined with reference to the % of the population of the oligonucleotide which retains the desired stereodefined internucleoside linkage motif(s), the stereorandom linkages being disregarded in the calculation.

Nucleobase

The term nucleobase includes the purine (e.g. adenine and guanine) and pyrimidine (e.g. uracil, thymine and cytosine) moieties present in nucleosides and nucleotides which form hydrogen bonds in nucleic acid hybridization. In the context of the present invention the term nucleobase also encompasses modified nucleobases which may differ from naturally occurring nucleobases, but are functional during nucleic acid hybridization. In this context “nucleobase” refers to both naturally occurring nucleobases such as adenine, guanine, cytosine, thymidine, uracil, xanthine and hypoxanthine, as well as non-naturally occurring variants. Such variants are for example described in Hirao et al (2012) Accounts of Chemical Research vol 45 page 2055 and Bergstrom (2009) Current Protocols in Nucleic Acid Chemistry Suppl. 37 1.4.1.

In some embodiments the nucleobase moiety is modified by changing the purine or pyrimidine into a modified purine or pyrimidine, such as substituted purine or substituted pyrimidine, such as a nucleobase selected from isocytosine, pseudoisocytosine, 5-methyl cytosine, 5-thiozolo-cytosine, 5-propynyl-cytosine, 5-propynyl-uracil, 5-bromouracil 5-thiazolo-uracil, 2-thio-uracil, 2'-thio-thymine, inosine, diaminopurine, 6-aminopurine, 2-aminopurine, 2,6-diaminopurine and 2-chloro-6-aminopurine.

The nucleobase moieties may be indicated by the letter code for each corresponding nucleobase, e.g. A, T, G, C or U, wherein each letter may optionally include modified nucleobases of equivalent function. For example, in the exemplified oligonucleotides, the nucleobase moieties are selected from A, T, G, C, and 5-methyl cytosine. Optionally, for LNA gapmers, 5-methyl cytosine LNA nucleosides may be used.

Modified oligonucleotide

The term modified oligonucleotide describes an oligonucleotide comprising one or more sugar-modified nucleosides and/or modified internucleoside linkages. The term "chimeric" oligonucleotide is a term that has been used in the literature to describe oligonucleotides with modified nucleosides.

5 ***Stereodefined oligonucleotide***

A stereodefined oligonucleotide is an oligonucleotide wherein at least one of the internucleoside linkages is a stereodefined internucleoside linkage.

A stereodefined phosphorothioate oligonucleotide is an oligonucleotide wherein at least one of the internucleoside linkages is a stereodefined phosphorothioate
10 internucleoside linkage.

Complementarity

The term "complementarity" describes the capacity for Watson-Crick base-pairing of nucleosides/nucleotides. Watson-Crick base pairs are guanine (G)-cytosine (C) and adenine (A) - thymine (T)/uracil (U). It will be understood that oligonucleotides may
15 comprise nucleosides with modified nucleobases, for example 5-methyl cytosine is often used in place of cytosine, and as such the term complementarity encompasses Watson Crick base-pairing between non-modified and modified nucleobases (see for example Hirao et al (2012) Accounts of Chemical Research vol 45 page 2055 and Bergstrom (2009) Current Protocols in Nucleic Acid Chemistry Suppl. 37 1.4.1).

20 The term "% complementary" as used herein, refers to the proportion of nucleotides in a contiguous nucleotide sequence in a nucleic acid molecule (e.g. oligonucleotide) which, at a given position, are complementary to (*i.e.* form Watson Crick base pairs with) a contiguous nucleotide sequence, at a given position of a separate nucleic acid molecule (e.g. the target nucleic acid). The percentage is calculated by counting the number of
25 aligned bases that form pairs between the two sequences (when aligned with the target sequence 5'-3' and the oligonucleotide sequence from 3'-5'), dividing by the total number of nucleotides in the oligonucleotide and multiplying by 100. In such a comparison a nucleobase/nucleotide which does not align (form a base pair) is termed a mismatch. Preferably, insertions and deletions are not allowed in the calculation of %
30 complementarity of a contiguous nucleotide sequence.

The term "fully complementary", refers to 100% complementarity.

Identity

The term “Identity” as used herein, refers to the number of nucleotides in percent of a contiguous nucleotide sequence in a nucleic acid molecule (e.g. oligonucleotide) which, at a given position, are identical to (*i.e.* in their ability to form Watson Crick base pairs with the complementary nucleoside) a contiguous nucleotide sequence, at a given position of a separate nucleic acid molecule (e.g. the target nucleic acid). The percentage is calculated by counting the number of aligned bases that are identical between the two sequences dividing by the total number of nucleotides in the oligonucleotide and multiplying by 100. Percent Identity = (Matches x 100)/Length of aligned region. Preferably, insertions and deletions are not allowed in the calculation of % complementarity of a contiguous nucleotide sequence.

Hybridization

The term “hybridizing” or “hybridizes” as used herein is to be understood as two nucleic acid strands (e.g. an oligonucleotide and a target nucleic acid) forming hydrogen bonds between base pairs on opposite strands thereby forming a duplex. The affinity of the binding between two nucleic acid strands is the strength of the hybridization. It is often described in terms of the melting temperature (T_m) defined as the temperature at which half of the oligonucleotides are duplexed with the target nucleic acid. At physiological conditions T_m is not strictly proportional to the affinity (Mergny and Lacroix, 2003, *Oligonucleotides* 13:515–537). The standard state Gibbs free energy ΔG° is a more accurate representation of binding affinity and is related to the dissociation constant (K_d) of the reaction by $\Delta G^\circ = -RT \ln(K_d)$, where R is the gas constant and T is the absolute temperature. Therefore, a very low ΔG° of the reaction between an oligonucleotide and the target nucleic acid reflects a strong hybridization between the oligonucleotide and target nucleic acid. ΔG° is the energy associated with a reaction where aqueous concentrations are 1M, the pH is 7, and the temperature is 37°C. The hybridization of oligonucleotides to a target nucleic acid is a spontaneous reaction and for spontaneous reactions ΔG° is less than zero. ΔG° can be measured experimentally, for example, by use of the isothermal titration calorimetry (ITC) method as described in Hansen et al., 1965, *Chem. Comm.* 36–38 and Holdgate et al., 2005, *Drug Discov Today*. The skilled person will know that commercial equipment is available for ΔG° measurements. ΔG° can also be estimated numerically by using the nearest neighbor model as described by SantaLucia, 1998, *Proc Natl Acad Sci USA*. 95: 1460–1465 using appropriately derived thermodynamic parameters described by Sugimoto et al., 1995, *Biochemistry* 34:11211–11216 and McTigue et al., 2004, *Biochemistry* 43:5388–5405. In order to have the possibility of modulating its intended nucleic acid target by hybridization, oligonucleotides of the present invention hybridize to a target nucleic acid with estimated ΔG° values below -10 kcal for oligonucleotides that are 10-30 nucleotides in length. In some embodiments the degree or strength of hybridization is measured by the standard state Gibbs free energy

ΔG° . The oligonucleotides may hybridize to a target nucleic acid with estimated ΔG° values below the range of -10 kcal, such as below -15 kcal, such as below -20 kcal and such as below -25 kcal for oligonucleotides that are 8-30 nucleotides in length. In some embodiments the oligonucleotides hybridize to a target nucleic acid with an estimated ΔG° value of -10 to -60 kcal, such as -12 to -40, such as from -15 to -30 kcal or -16 to -27 kcal such as -18 to -25 kcal.

Sugar modifications

The oligomer of the invention may comprise one or more nucleosides which have a modified sugar moiety, *i.e.* a modification of the sugar moiety when compared to the ribose sugar moiety found in DNA and RNA.

Numerous nucleosides with modification of the ribose sugar moiety have been made, primarily with the aim of improving certain properties of oligonucleotides, such as affinity and/or nuclease resistance.

Such modifications include those where the ribose ring structure is modified, *e.g.* by replacement with a hexose ring (HNA), or a bicyclic ring, which typically have a biradical bridge between the C2 and C4 carbons on the ribose ring (LNA), or an unlinked ribose ring which typically lacks a bond between the C2 and C3 carbons (*e.g.* UNA). Other sugar modified nucleosides include, for example, bicyclohexose nucleic acids (WO 2011/017521) or tricyclic nucleic acids (WO 2013/154798). Modified nucleosides also include nucleosides where the sugar moiety is replaced with a non-sugar moiety, for example in the case of peptide nucleic acids (PNA), or morpholino nucleic acids.

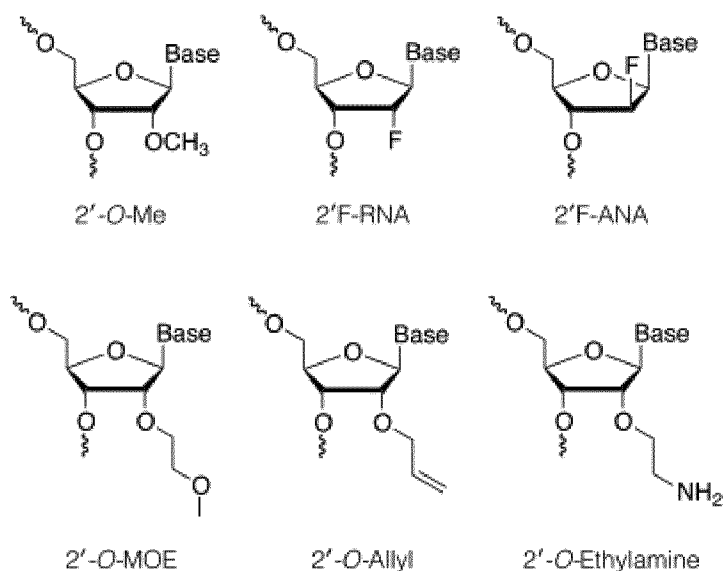
Sugar modifications also include modifications made via altering the substituent groups on the ribose ring to groups other than hydrogen, or the 2'-OH group naturally found in DNA and RNA nucleosides. Substituents may, for example be introduced at the 2', 3', 4' or 5' positions.

2' sugar modified nucleosides.

A 2' sugar modified nucleoside is a nucleoside which has a substituent other than H or -OH at the 2' position (2' substituted nucleoside) or comprises a 2' linked biradical capable of forming a bridge between the 2' carbon and a second carbon in the ribose ring, such as LNA (2' - 4' biradical bridged) nucleosides.

Indeed, much focus has been spent on developing 2' substituted nucleosides, and numerous 2' substituted nucleosides have been found to have beneficial properties when incorporated into oligonucleotides. For example, the 2' modified sugar may provide enhanced binding affinity and/or increased nuclease resistance to the oligonucleotide.

Examples of 2' substituted modified nucleosides are 2'-O-alkyl-RNA, 2'-O-methyl-RNA, 2'-alkoxy-RNA, 2'-O-methoxyethyl-RNA (MOE), 2'-amino-DNA, 2'-fluoro-RNA and 2'-F-ANA nucleoside. Further examples can be found in e.g. Freier & Altmann; Nucl. Acid Res., 1997, 25, 4429-4443 and Uhlmann; Curr. Opinion in Drug Development, 2000, 3(2), 293-213 and Deleavey and Damha, Chemistry and Biology 2012, 19, 937. Below are illustrations of some 2' substituted modified nucleosides.



In relation to the present invention 2' substituted does not include 2' bridged molecules like LNA.

Locked Nucleic Acid Nucleosides (LNA nucleosides)

A "LNA nucleoside" is a 2'-modified nucleoside which comprises a biradical linking the C2' and C4' of the ribose sugar ring of said nucleoside (also referred to as a "2'-4' bridge"), which restricts or locks the conformation of the ribose ring. These nucleosides are also termed bridged nucleic acid or bicyclic nucleic acid (BNA) in the literature. The locking of the conformation of the ribose is associated with an enhanced affinity of hybridization (duplex stabilization) when the LNA is incorporated into an oligonucleotide for a complementary RNA or DNA molecule. This can be routinely determined by measuring the melting temperature of the oligonucleotide/complement duplex.

Non limiting, exemplary LNA nucleosides are disclosed in WO 99/014226, WO 00/66604, WO 98/039352, WO 2004/046160, WO 00/047599, WO 2007/134181, WO 2010/077578, WO 2010/036698, WO 2007/090071, WO 2009/006478, WO 2011/156202, WO 2008/154401, WO 2009/067647, WO 2008/150729, Morita et al., Bioorganic &

Med.Chem. Lett. 12, 73-76, Seth et al. J. Org. Chem. 2010, Vol 75(5) pp. 1569-81 and Mitsuoka et al., Nucleic Acids Research 2009, 37(4), 1225-1238.

The 2'-4' bridge comprises 2 to 4 bridging atoms and is in particular of formula -X-Y-, X being linked to C4' and Y linked to C2',

5 wherein

X is oxygen, sulfur, $-CR^aR^b-$, $-C(R^a)=C(R^b)-$, $-C(=CR^aR^b)-$, $-C(R^a)=N-$, $-Si(R^a)_2-$, $-SO_2-$, $-NR^a-$, $-O-NR^a-$, $-NR^a-O-$, $-C(=J)-$, Se, $-O-NR^a-$, $-NR^a-CR^aR^b-$, $-N(R^a)-O-$ or $-O-CR^aR^b-$;

10 Y is oxygen, sulfur, $-(CR^aR^b)_n-$, $-CR^aR^b-O-CR^aR^b-$, $-C(R^a)=C(R^b)-$, $-C(R^a)=N-$, $-Si(R^a)_2-$, $-SO_2-$, $-NR^a-$, $-C(=J)-$, Se, $-O-NR^a-$, $-NR^a-CR^aR^b-$, $-N(R^a)-O-$ or $-O-CR^aR^b-$;

with the proviso that -X-Y- is not $-O-O-$, $Si(R^a)_2-Si(R^a)_2-$, $-SO_2-SO_2-$, $-C(R^a)=C(R^b)-C(R^a)=C(R^b)-$, $-C(R^a)=N-C(R^a)=N-$, $-C(R^a)=N-C(R^a)=C(R^b)-$, $-C(R^a)=C(R^b)-C(R^a)=N-$ or $-Se-Se-$;

15 J is oxygen, sulfur, $=CH_2$ or $=N(R^a)$;

R^a and R^b are independently selected from hydrogen, halogen, hydroxyl, cyano, thiohydroxyl, alkyl, substituted alkyl, alkenyl, substituted alkenyl, alkynyl, substituted alkynyl, alkoxy, substituted alkoxy, alkoxyalkyl, alkenyloxy, carboxyl, alkoxycarbonyl, alkylcarbonyl, formyl, aryl, heterocyclyl, amino, 20 alkylamino, carbamoyl, alkylaminocarbonyl, aminoalkylaminocarbonyl, alkylaminoalkylaminocarbonyl, alkylcarbonylamino, carbamido, alkanoyloxy, sulfonyl, alkylsulfonyloxy, nitro, azido, thiohydroxylsulfidealkylsulfanyl, aryloxycarbonyl, aryloxy, arylcarbonyl, heteroaryl, heteroaryloxycarbonyl, heteroaryloxy, heteroarylcarbonyl, $-OC(=X^a)R^c$, $-OC(=X^a)NR^cR^d$ and - 25 $NR^cC(=X^a)NR^cR^d$;

or two geminal R^a and R^b together form optionally substituted methylene;

or two geminal R^a and R^b , together with the carbon atom to which they are attached, form cycloalkyl or halocycloalkyl, with only one carbon atom of -X-Y-;

30 wherein substituted alkyl, substituted alkenyl, substituted alkynyl, substituted alkoxy and substituted methylene are alkyl, alkenyl, alkynyl and methylene substituted with 1 to 3 substituents independently selected from halogen, hydroxyl, alkyl, alkenyl, alkynyl, alkoxy, alkoxyalkyl, alkenyloxy, carboxyl, alkoxycarbonyl, alkylcarbonyl, formyl, heterocyclyl, aryl and heteroaryl;

X^a is oxygen, sulfur or -NR^c;

R^c, R^d and R^e are independently selected from hydrogen and alkyl; and

n is 1, 2 or 3.

In a further particular embodiment of the invention, X is oxygen, sulfur, -NR^a-, -
5 CR^aR^b- or -C(=CR^aR^b)-, particularly oxygen, sulfur, -NH-, -CH₂- or -C(=CH₂)-, more particularly oxygen.

In another particular embodiment of the invention, Y is -CR^aR^b-, -CR^aR^b-CR^aR^b- or -
CR^aR^b-CR^aR^b-CR^aR^b-, particularly -CH₂-CHCH₃-, -CHCH₃-CH₂-, -CH₂-CH₂- or -CH₂-
CH₂-CH₂-.

10 In a particular embodiment of the invention, -X-Y- is -O-(CR^aR^b)_n-, -S-CR^aR^b-, -
N(R^a)CR^aR^b-, -CR^aR^b-CR^aR^b-, -O-CR^aR^b-O-CR^aR^b-, -CR^aR^b-O-CR^aR^b-, -C(=CR^aR^b)-
CR^aR^b-, -N(R^a)CR^aR^b-, -O-N(R^a)-CR^aR^b- or -N(R^a)-O-CR^aR^b-.

In a particular embodiment of the invention, R^a and R^b are independently selected
from the group consisting of hydrogen, halogen, hydroxyl, alkyl and alkoxyalkyl, in
15 particular hydrogen, halogen, alkyl and alkoxyalkyl.

In another embodiment of the invention, R^a and R^b are independently selected from
the group consisting of hydrogen, fluoro, hydroxyl, methyl and -CH₂-O-CH₃, in particular
hydrogen, fluoro, methyl and -CH₂-O-CH₃.

Advantageously, one of R^a and R^b of -X-Y- is as defined above and the other ones
20 are all hydrogen at the same time.

In a further particular embodiment of the invention, R^a is hydrogen or alkyl, in
particular hydrogen or methyl.

In another particular embodiment of the invention, R^b is hydrogen or or alkyl, in
particular hydrogen or methyl.

25 In a particular embodiment of the invention, one or both of R^a and R^b are hydrogen.

In a particular embodiment of the invention, only one of R^a and R^b is hydrogen.

In one particular embodiment of the invention, one of R^a and R^b is methyl and the
other one is hydrogen.

In a particular embodiment of the invention, R^a and R^b are both methyl at the same
30 time.

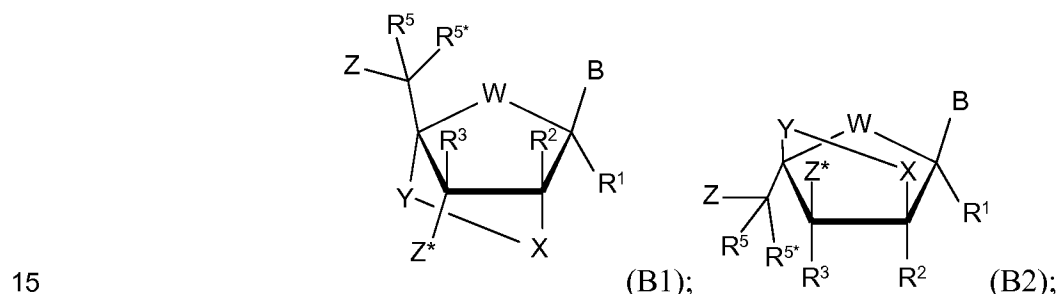
In a particular embodiment of the invention, -X-Y- is -O-CH₂-, -S-CH₂-, -S-CH(CH₃)-, -NH-CH₂-, -O-CH₂CH₂-, -O-CH(CH₂-O-CH₃)-, -O-CH(CH₂CH₃)-, -O-CH(CH₃)-, -O-CH₂-O-CH₂-, -O-CH₂-O-CH₂-, -CH₂-O-CH₂-, -C(=CH₂)CH₂-, -C(=CH₂)CH(CH₃)-, -N(OCH₃)CH₂- or -N(CH₃)CH₂-;

- 5 In a particular embodiment of the invention, -X-Y- is -O-CR^aR^b- wherein R^a and R^b are independently selected from the group consisting of hydrogen, alkyl and alkoxyalkyl, in particular hydrogen, methyl and -CH₂-O-CH₃.

In a particular embodiment, -X-Y- is -O-CH₂- or -O-CH(CH₃)-, particularly -O-CH₂-

- 10 The 2'-4' bridge may be positioned either below the plane of the ribose ring (beta-D- configuration), or above the plane of the ring (alpha-L- configuration), as illustrated in formula (A) and formula (B) respectively.

The LNA nucleoside according to the invention is in particular of formula (B1) or (B2)



wherein

W is oxygen, sulfur, -N(R^a)- or -CR^aR^b-, in particular oxygen;

B is a nucleobase or a modified nucleobase;

Z is an internucleoside linkage to an adjacent nucleoside or a 5'-terminal group;

- 20 Z* is an internucleoside linkage to an adjacent nucleoside or a 3'-terminal group;

R¹, R², R³, R⁵ and R^{5*} are independently selected from hydrogen, halogen, alkyl, haloalkyl, alkenyl, alkynyl, hydroxy, alkoxy, alkoxyalkyl, azido, alkenyloxy, carboxyl, alkoxycarbonyl, alkylcarbonyl, formyl and aryl; and

X, Y, R^a and R^b are as defined above.

- 25 In a particular embodiment, in the definition of -X-Y-, R^a is hydrogen or alkyl, in particular hydrogen or methyl. In another particular embodiment, in the definition of -X-

Y-, R^b is hydrogen or alkyl, in particular hydrogen or methyl. In a further particular embodiment, in the definition of -X-Y-, one or both of R^a and R^b are hydrogen. In a particular embodiment, in the definition of -X-Y-, only one of R^a and R^b is hydrogen. In one particular embodiment, in the definition of -X-Y-, one of R^a and R^b is methyl and the
5 other one is hydrogen. In a particular embodiment, in the definition of -X-Y-, R^a and R^b are both methyl at the same time.

In a further particular embodiment, in the definition of X, R^a is hydrogen or alkyl, in particular hydrogen or methyl. In another particular embodiment, in the definition of X, R^b is hydrogen or alkyl, in particular hydrogen or methyl. In a particular embodiment, in the
10 definition of X, one or both of R^a and R^b are hydrogen. In a particular embodiment, in the definition of X, only one of R^a and R^b is hydrogen. In one particular embodiment, in the definition of X, one of R^a and R^b is methyl and the other one is hydrogen. In a particular embodiment, in the definition of X, R^a and R^b are both methyl at the same time.

In a further particular embodiment, in the definition of Y, R^a is hydrogen or alkyl, in particular hydrogen or methyl. In another particular embodiment, in the definition of Y, R^b is hydrogen or alkyl, in particular hydrogen or methyl. In a particular embodiment, in the
15 definition of Y, one or both of R^a and R^b are hydrogen. In a particular embodiment, in the definition of Y, only one of R^a and R^b is hydrogen. In one particular embodiment, in the definition of Y, one of R^a and R^b is methyl and the other one is hydrogen. In a particular
20 embodiment, in the definition of Y, R^a and R^b are both methyl at the same time.

In a particular embodiment of the invention R¹, R², R³, R⁵ and R^{5*} are independently selected from hydrogen and alkyl, in particular hydrogen and methyl.

In a further particular advantageous embodiment of the invention, R¹, R², R³, R⁵ and R^{5*} are all hydrogen at the same time.

25 In another particular embodiment of the invention, R¹, R², R³, are all hydrogen at the same time, one of R⁵ and R^{5*} is hydrogen and the other one is as defined above, in particular alkyl, more particularly methyl.

In a particular embodiment of the invention, R⁵ and R^{5*} are independently selected from hydrogen, halogen, alkyl, alkoxyalkyl and azido, in particular from hydrogen, fluoro,
30 methyl, methoxyethyl and azido. In particular advantageous embodiments of the invention, one of R⁵ and R^{5*} is hydrogen and the other one is alkyl, in particular methyl, halogen, in particular fluoro, alkoxyalkyl, in particular methoxyethyl or azido; or R⁵ and R^{5*} are both hydrogen or halogen at the same time, in particular both hydrogen or fluoro at the same time. In such particular embodiments, W can advantageously be oxygen, and -X-Y-
35 advantageously -O-CH₂-.

In a particular embodiment of the invention, -X-Y- is -O-CH₂-, W is oxygen and R¹, R², R³, R⁵ and R^{5*} are all hydrogen at the same time. Such LNA nucleosides are disclosed in WO 99/014226, WO 00/66604, WO 98/039352 and WO 2004/046160 which are all hereby incorporated by reference, and include what are commonly known in the art as
5 beta-D-oxy LNA and alpha-L-oxy LNA nucleosides.

In another particular embodiment of the invention, -X-Y- is -S-CH₂-, W is oxygen and R¹, R², R³, R⁵ and R^{5*} are all hydrogen at the same time. Such thio LNA nucleosides are disclosed in WO 99/014226 and WO 2004/046160 which are hereby incorporated by reference.

10 In another particular embodiment of the invention, -X-Y- is -NH-CH₂-, W is oxygen and R¹, R², R³, R⁵ and R^{5*} are all hydrogen at the same time. Such amino LNA nucleosides are disclosed in WO 99/014226 and WO 2004/046160 which are hereby incorporated by reference.

In another particular embodiment of the invention, -X-Y- is -O-CH₂CH₂- or -
15 OCH₂CH₂CH₂-, W is oxygen, and R¹, R², R³, R⁵ and R^{5*} are all hydrogen at the same time. Such LNA nucleosides are disclosed in WO 00/047599 and Morita *et al.*, Bioorganic & Med.Chem. Lett. 12, 73-76, which are hereby incorporated by reference, and include what are commonly known in the art as 2'-O-4'C-ethylene bridged nucleic acids (ENA).

In another particular embodiment of the invention, -X-Y- is -O-CH₂-, W is oxygen,
20 R¹, R², R³ are all hydrogen at the same time, one of R⁵ and R^{5*} is hydrogen and the other one is not hydrogen, such as alkyl, for example methyl. Such 5' substituted LNA nucleosides are disclosed in WO 2007/134181 which is hereby incorporated by reference.

In another particular embodiment of the invention, -X-Y- is -O-CR^aR^b-, wherein one or both of R^a and R^b are not hydrogen, in particular alkyl such as methyl, W is oxygen, R¹,
25 R², R³ are all hydrogen at the same time, one of R⁵ and R^{5*} is hydrogen and the other one is not hydrogen, in particular alkyl, for example methyl. Such bis modified LNA nucleosides are disclosed in WO 2010/077578 which is hereby incorporated by reference.

In another particular embodiment of the invention, -X-Y- is -O-CHR^a-, W is oxygen and R¹, R², R³, R⁵ and R^{5*} are all hydrogen at the same time. Such 6'-substituted LNA
30 nucleosides are disclosed in WO 2010/036698 and WO 2007/090071 which are both hereby incorporated by reference. In such 6'-substituted LNA nucleosides, R^a is in particular C₁-C₆ alkyl, such as methyl.

In another particular embodiment of the invention, -X-Y- is -O-CH(CH₂-O-CH₃)-
35 ("2' O-methoxyethyl bicyclic nucleic acid", Seth *et al.* J. Org. Chem. 2010, Vol 75(5) pp. 1569-81).

In another particular embodiment of the invention, -X-Y- is -O-CH(CH₂CH₃)-;

In another particular embodiment of the invention, -X-Y- is -O-CH(CH₂-O-CH₃)-, W is oxygen and R¹, R², R³, R⁵ and R^{5*} are all hydrogen at the same time. Such LNA nucleosides are also known in the art as cyclic MOEs (cMOE) and are disclosed in WO
5 2007/090071.

In another particular embodiment of the invention, -X-Y- is -O-CH(CH₃)- (“2’O-ethyl bicyclic nucleic acid”, *Seth et al.*, J. Org. Chem. 2010, Vol 75(5) pp. 1569-81).

In another particular embodiment of the invention, -X-Y- is -O-CH₂-O-CH₂- (*Seth et al.*, J. Org. Chem 2010 op. cit.)

10 In another particular embodiment of the invention, -X-Y- is -O-CH(CH₃)-, W is oxygen and R¹, R², R³, R⁵ and R^{5*} are all hydrogen at the same time. Such 6’-methyl LNA nucleosides are also known in the art as cET nucleosides, and may be either (S)-cET or (R)-cET diastereoisomers, as disclosed in WO 2007/090071 (beta-D) and WO 2010/036698 (alpha-L) which are both hereby incorporated by reference.

15 In another particular embodiment of the invention, -X-Y- is -O-CR^aR^b-, wherein neither R^a nor R^b is hydrogen, W is oxygen and R¹, R², R³, R⁵ and R^{5*} are all hydrogen at the same time. In a particular embodiment, R^a and R^b are both alkyl at the same time, in particular both methyl at the same time. Such 6’-di-substituted LNA nucleosides are disclosed in WO 2009/006478 which is hereby incorporated by reference.

20 In another particular embodiment of the invention, -X-Y- is -S-CHR^a-, W is oxygen and R¹, R², R³, R⁵ and R^{5*} are all hydrogen at the same time. Such 6’-substituted thio LNA nucleosides are disclosed in WO 2011/156202 which is hereby incorporated by reference. In a particular embodiment of such 6’-substituted thio LNA, R^a is alkyl, in particular methyl.

25 In a particular embodiment of the invention, -X-Y- is -C(=CH₂)C(R^aR^b)-, -C(=CHF)C(R^aR^b)- or -C(=CF₂)C(R^aR^b)-, W is oxygen and R¹, R², R³, R⁵ and R^{5*} are all hydrogen at the same time. R^a and R^b are advantageously independently selected from hydrogen, halogen, alkyl and alkoxyalkyl, in particular hydrogen, methyl, fluoro and methoxymethyl. R^a and R^b are in particular both hydrogen or methyl at the same time or
30 one of R^a and R^b is hydrogen and the other one is methyl. Such vinyl carbo LNA nucleosides are disclosed in WO 2008/154401 and WO 2009/067647 which are both hereby incorporated by reference.

In a particular embodiment of the invention, -X-Y- is -N(OR^a)-CH₂-, W is oxygen and R¹, R², R³, R⁵ and R^{5*} are all hydrogen at the same time. In a particular embodiment,

R^a is alkyl such as methyl. Such LNA nucleosides are also known as N substituted LNAs and are disclosed in WO 2008/150729 which is hereby incorporated by reference.

In a particular embodiment of the invention, -X-Y- is -O-N(R^a)-, -N(R^a)-O-, -NR^a-CR^aR^b-CR^aR^b- or -NR^a-CR^aR^b-, W is oxygen and R¹, R², R³, R⁵ and R^{5*} are all hydrogen at the same time. R^a and R^b are advantageously independently selected from hydrogen, halogen, alkyl and alkoxyalkyl, in particular hydrogen, methyl, fluoro and methoxymethyl. In a particular embodiment, R^a is alkyl, such as methyl, R^b is hydrogen or methyl, in particular hydrogen. (Seth *et al.*, J. Org. Chem 2010 op. cit.).

In a particular embodiment of the invention, -X-Y- is -O-N(CH₃)- (Seth *et al.*, J. Org. Chem 2010 op. cit.).

In a particular embodiment of the invention, R⁵ and R^{5*} are both hydrogen at the same time. In another particular embodiment of the invention, one of R⁵ and R^{5*} is hydrogen and the other one is alkyl, such as methyl. In such embodiments, R¹, R² and R³ can be in particular hydrogen and -X-Y- can be in particular -O-CH₂- or -O-CHC(R^a)₃-, such as -O-CH(CH₃)-.

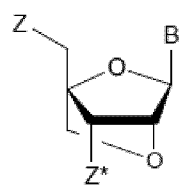
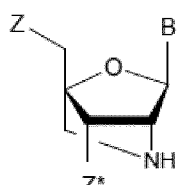
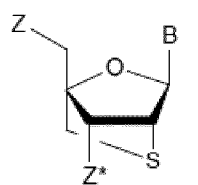
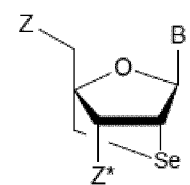
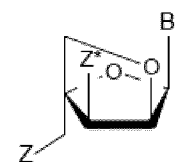
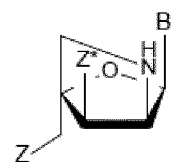
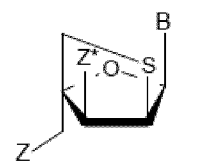
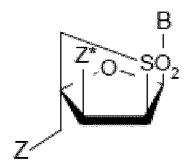
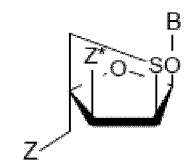
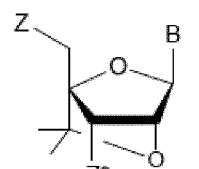
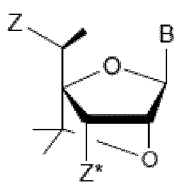
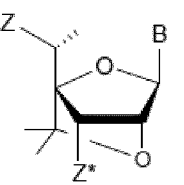
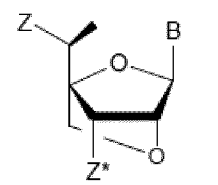
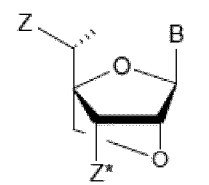
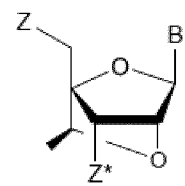
In a particular embodiment of the invention, -X-Y- is -CR^aR^b-O-CR^aR^b-, such as -CH₂-O-CH₂-, W is oxygen and R¹, R², R³, R⁵ and R^{5*} are all hydrogen at the same time. In such particular embodiments, R^a can be in particular alkyl such as methyl, R^b hydrogen or methyl, in particular hydrogen. Such LNA nucleosides are also known as conformationally restricted nucleotides (CRNs) and are disclosed in WO 2013/036868 which is hereby incorporated by reference.

In a particular embodiment of the invention, -X-Y- is -O-CR^aR^b-O-CR^aR^b-, such as -O-CH₂-O-CH₂-, W is oxygen and R¹, R², R³, R⁵ and R^{5*} are all hydrogen at the same time. R^a and R^b are advantageously independently selected from hydrogen, halogen, alkyl and alkoxyalkyl, in particular hydrogen, methyl, fluoro and methoxymethyl. In such a particular embodiment, R^a can be in particular alkyl such as methyl, R^b hydrogen or methyl, in particular hydrogen. Such LNA nucleosides are also known as COC nucleotides and are disclosed in Mitsuoka *et al.*, Nucleic Acids Research 2009, 37(4), 1225-1238, which is hereby incorporated by reference.

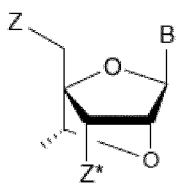
It will be recognized than, unless specified, the LNA nucleosides may be in the beta-D or alpha-L stereoisofom.

Particular examples of LNA nucleosides of the invention are presented in Scheme 1 (wherein B is as defined above).

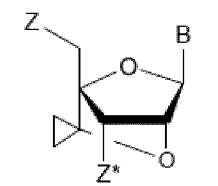
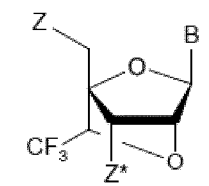
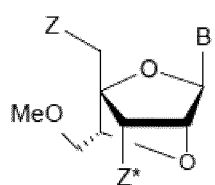
Scheme 1

 β -D-oxy LNA β -D-amino LNA β -D-thio LNA β -D-Se LNA α -L-oxy LNA α -L-amino LNA α -L-thio LNAcarbocyclic(vinyl)
 α -L LNA6'-dimethyl- β -D
-oxy LNA(S)-5'-methyl-6'-di
methyl- β -D-oxy LNA(R)-5'-methyl-6'-di
methyl- β -D-oxy LNA(S)-5'-methyl- β -D
-oxy LNA(R)-5'-methyl- β -D
-oxy LNA

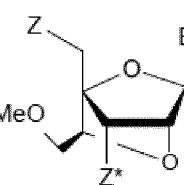
(S)-cET



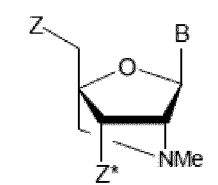
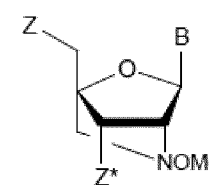
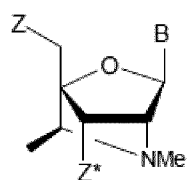
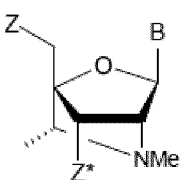
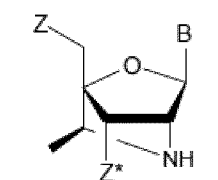
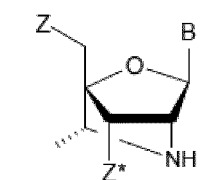
(R)-cET

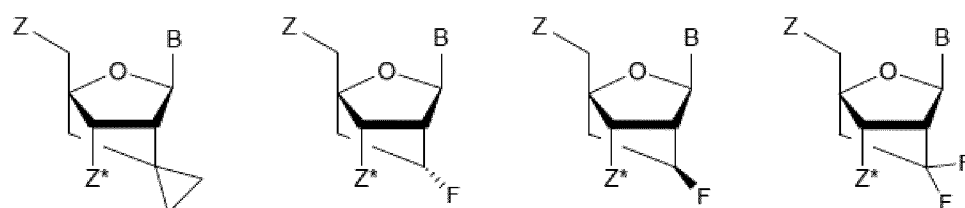
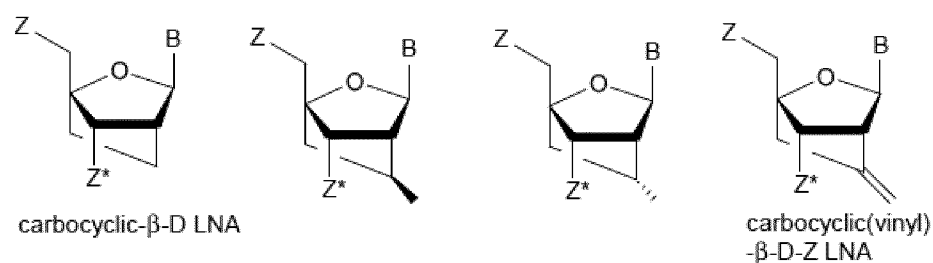
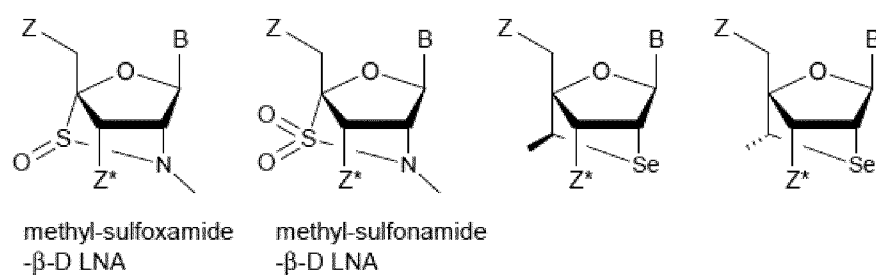
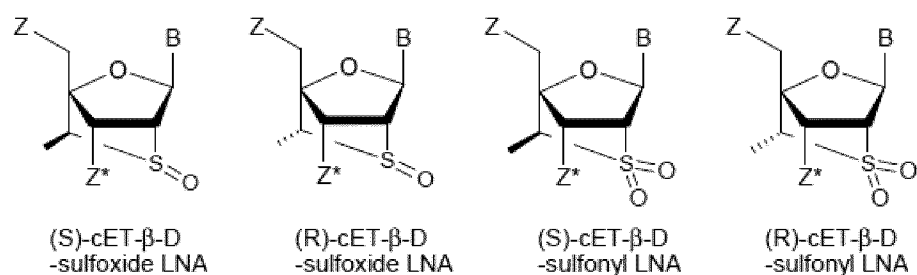
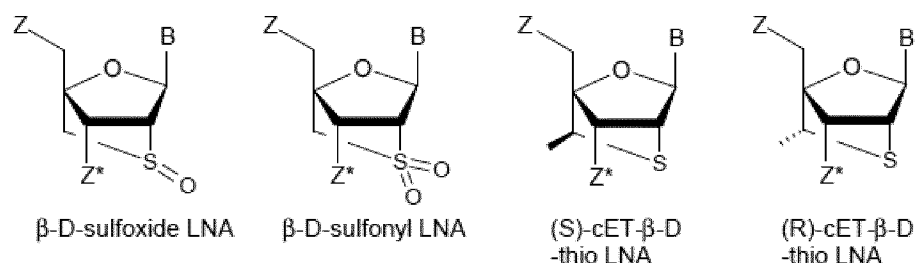
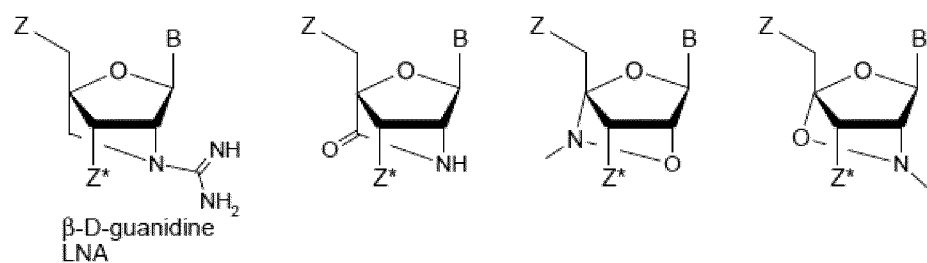
cprop- β -D-oxy LNAtrifluoromethyl
- β -D-oxy LNA

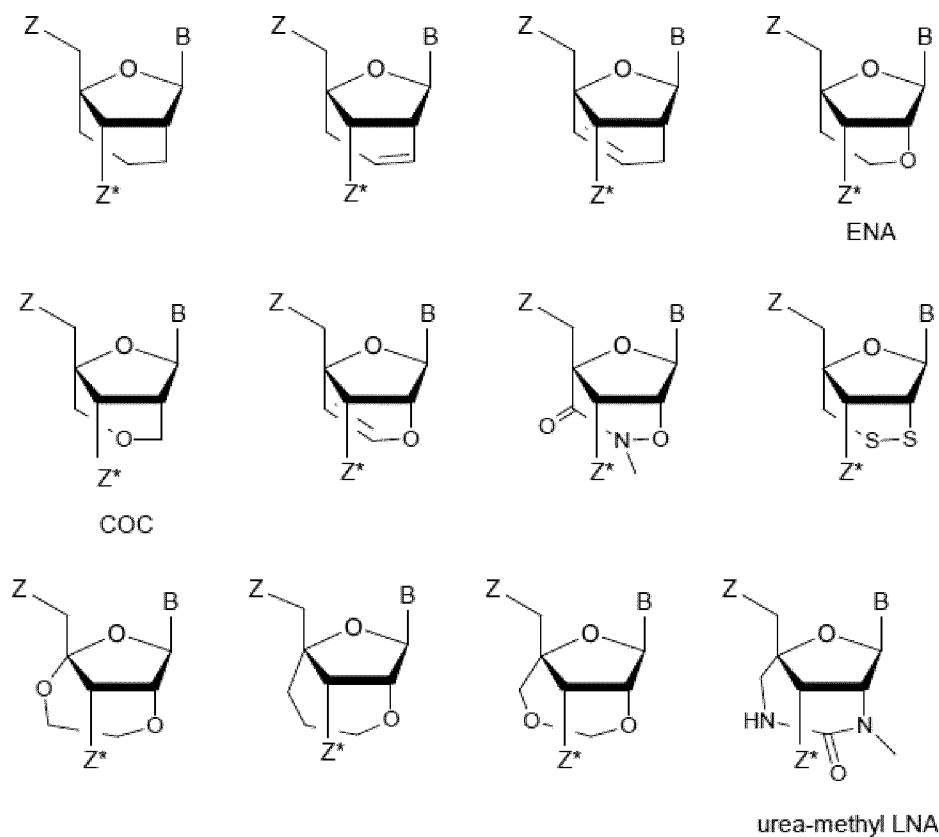
(R)-cMOE



(S)-cMOE

 β -D-methylamino
LNA β -D-methoxyamino
LNA β -D-(S)-cET
-methylamino LNA β -D-(R)-cET
-methylamino LNA β -D-(S)-cET
-amino LNA β -D-(R)-cET
-amino LNA

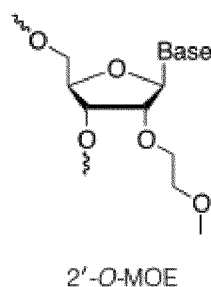




Particular LNA nucleosides are beta-D-oxy-LNA, 6'-methyl-beta-D-oxy LNA such
 5 as (S)-6'-methyl-beta-D-oxy-LNA ((S)-cET) and ENA.

MOE nucleoside

The term “MOE” stands for “methoxy-ethyl” and refers by means of abbreviation to
 a nucleoside substituted in 2' position with a methoxy-ethoxy group as represented below.



10 The above nucleoside can thus be named either “MOE” or “2'-O-MOE nucleoside”.

RNase H Activity and Recruitment

The RNase H activity of an antisense oligonucleotide refers to its ability to recruit
 RNase H when in a duplex with a complementary RNA molecule. WO01/23613 provides
in vitro methods for determining RNaseH activity, which may be used to determine the

ability to recruit RNaseH. Typically an oligonucleotide is deemed capable of recruiting RNase H if it, when provided with a complementary target nucleic acid sequence, has an initial rate, as measured in pmol/l/min, of at least 5%, such as at least 10% or more than 20% of the of the initial rate determined when using a oligonucleotide having the same
5 base sequence as the modified oligonucleotide being tested, but containing only DNA monomers with phosphorothioate linkages between all monomers in the oligonucleotide, and using the methodology provided by Example 91 - 95 of WO01/23613 (hereby incorporated by reference). For use in determining RNase H activity, recombinant human RNase H1 is available from Lubio Science GmbH, Lucerne, Switzerland.

10 *Gapmer*

The antisense oligonucleotide of the invention, or contiguous nucleotide sequence thereof may be a gapmer. The antisense gapmers are commonly used to inhibit a target nucleic acid via RNase H mediated degradation. A gapmer oligonucleotide comprises at least three distinct structural regions a 5'-flank, a gap and a 3'-flank, F-G-F' in the '5 -> 3'
15 orientation. The "gap" region (G) comprises a stretch of contiguous DNA nucleotides which enable the oligonucleotide to recruit RNase H. The gap region is flanked by a 5' flanking region (F) comprising one or more sugar modified nucleosides, advantageously high affinity sugar modified nucleosides, and by a 3' flanking region (F') comprising one or more sugar modified nucleosides, advantageously high affinity sugar modified
20 nucleosides. The one or more sugar modified nucleosides in region F and F' enhance the affinity of the oligonucleotide for the target nucleic acid (*i.e.* are affinity enhancing sugar modified nucleosides). In some embodiments, the one or more sugar modified nucleosides in region F and F' are 2' sugar modified nucleosides, such as high affinity 2' sugar modifications, such as independently selected from LNA and 2'-MOE.

25 In a gapmer design, the 5' and 3' most nucleosides of the gap region are DNA nucleosides, and are positioned adjacent to a sugar modified nucleoside of the 5' (F) or 3' (F') region respectively. The flanks may further defined by having at least one sugar modified nucleoside at the end most distant from the gap region, *i.e.* at the 5' end of the 5' flank and at the 3' end of the 3' flank.

30 Regions F-G-F' form a contiguous nucleotide sequence. Antisense oligonucleotides of the invention, or the contiguous nucleotide sequence thereof, may comprise a gapmer region of formula F-G-F'.

The overall length of the gapmer design F-G-F' may be, for example 12 to 32 nucleosides, such as 13 to 24, such as 14 to 22 nucleosides, Such as from 14 to 17, such as
35 16 to 18 nucleosides.

By way of example, the gapmer oligonucleotide of the present invention can be represented by the following formulae:

F₁₋₈-G₅₋₁₆-F'₁₋₈, such as

F₁₋₈-G₇₋₁₆-F'₂₋₈

- 5 with the proviso that the overall length of the gapmer regions F-G-F' is at least 12, such as at least 14 nucleotides in length.

Regions F, G and F' are further defined below and can be incorporated into the F-G-F' formula.

Gapmer - Region G

- 10 Region G (gap region) of the gapmer is a region of nucleosides which enables the oligonucleotide to recruit RNaseH, such as human RNase H1, typically DNA nucleosides. RNaseH is a cellular enzyme which recognizes the duplex between DNA and RNA, and enzymatically cleaves the RNA molecule. Suitable gapmers may have a gap region (G) of at least 5 or 6 contiguous DNA nucleosides, such as 5 – 16 contiguous DNA nucleosides,
- 15 such as 6 – 15 contiguous DNA nucleosides, such as 7-14 contiguous DNA nucleosides, such as 8 – 12 contiguous DNA nucleotides, such as 8 – 12 contiguous DNA nucleotides in length. The gap region G may, in some embodiments consist of 6, 7, 8, 9, 10, 11, 12, 13, 14, 15 or 16 contiguous DNA nucleosides. Cytosine (C) DNA in the gap region may in some instances be methylated, such residues are either annotated as 5-methyl-cytosine
- 20 (^{me}C or with an e instead of a c). Methylation of Cytosine DNA in the gap is advantageous if cg dinucleotides are present in the gap to reduce potential toxicity, the modification does not have significant impact on efficacy of the oligonucleotides..

- In some embodiments the gap region G may consist of 6, 7, 8, 9, 10, 11, 12, 13, 14, 15 or 16 contiguous phosphorothioate linked DNA nucleosides. In some embodiments, all
- 25 internucleoside linkages in the gap are phosphorothioate linkages.

- Whilst traditional gapmers have a DNA gap region, there are numerous examples of modified nucleosides which allow for RNaseH recruitment when they are used within the gap region. Modified nucleosides which have been reported as being capable of recruiting RNaseH when included within a gap region include, for example, alpha-L-LNA, C4'
- 30 alkylated DNA (as described in PCT/EP2009/050349 and Vester *et al.*, Bioorg. Med. Chem. Lett. 18 (2008) 2296 – 2300, both incorporated herein by reference), arabinose derived nucleosides like ANA and 2'F-ANA (Mangos et al. 2003 J. AM. CHEM. SOC. 125, 654-661), UNA (unlocked nucleic acid) (as described in Fluiter *et al.*, Mol. Biosyst., 2009, 10, 1039 incorporated herein by reference). UNA is unlocked nucleic acid, typically

where the bond between C2 and C3 of the ribose has been removed, forming an unlocked “sugar” residue. The modified nucleosides used in such gapmers may be nucleosides which adopt a 2' endo (DNA like) structure when introduced into the gap region, *i.e.* modifications which allow for RNaseH recruitment). In some embodiments the DNA Gap region (G) described herein may optionally contain 1 to 3 sugar modified nucleosides which adopt a 2' endo (DNA like) structure when introduced into the gap region.

Region G - “Gap-breaker”

Alternatively, there are numerous reports of the insertion of a modified nucleoside which confers a 3' endo conformation into the gap region of gapmers, whilst retaining some RNaseH activity. Such gapmers with a gap region comprising one or more 3' endo modified nucleosides are referred to as “gap-breaker” or “gap-disrupted” gapmers, see for example WO2013/022984. Gap-breaker oligonucleotides retain sufficient region of DNA nucleosides within the gap region to allow for RNaseH recruitment. The ability of gapbreaker oligonucleotide design to recruit RNaseH is typically sequence or even compound specific – see Rukov et al. 2015 Nucl. Acids Res. Vol. 43 pp. 8476-8487, which discloses “gapbreaker” oligonucleotides which recruit RNaseH which in some instances provide a more specific cleavage of the target RNA. Modified nucleosides used within the gap region of gap-breaker oligonucleotides may for example be modified nucleosides which confer a 3' endo confirmation, such as 2' -O-methyl (OMe) or 2'-O-MOE (MOE) nucleosides, or beta-D LNA nucleosides (the bridge between C2' and C4' of the ribose sugar ring of a nucleoside is in the beta conformation), such as beta-D-oxy LNA or ScET nucleosides.

As with gapmers containing region G described above, the gap region of gap-breaker or gap-disrupted gapmers, have a DNA nucleosides at the 5' end of the gap (adjacent to the 3' nucleoside of region F), and a DNA nucleoside at the 3' end of the gap (adjacent to the 5' nucleoside of region F'). Gapmers which comprise a disrupted gap typically retain a region of at least 3 or 4 contiguous DNA nucleosides at either the 5' end or 3' end of the gap region.

Exemplary designs for gap-breaker oligonucleotides include

$F_{1-8}-[D_{3-4}-E_{1-} D_{3-4}]-F'_{1-8}$

$F_{1-8}-[D_{1-4}-E_{1-} D_{3-4}]-F'_{1-8}$

$F_{1-8}-[D_{3-4}-E_{1-} D_{1-4}]-F'_{1-8}$

wherein region G is within the brackets $[D_n-E_r- D_m]$, D is a contiguous sequence of DNA nucleosides, E is a modified nucleoside (the gap-breaker or gap-disrupting

nucleoside), and F and F' are the flanking regions as defined herein, and with the proviso that the overall length of the gapmer regions F-G-F' is at least 12, such as at least 14 nucleotides in length.

5 In some embodiments, region G of a gap disrupted gapmer comprises at least 6 DNA nucleosides, such as 6, 7, 8, 9, 10, 11, 12, 13, 14, 15 or 16 DNA nucleosides. As described above, the DNA nucleosides may be contiguous or may optionally be interspersed with one or more modified nucleosides, with the proviso that the gap region G is capable of mediating RNaseH recruitment.

Gapmer - flanking regions, F and F'

10 Region F is positioned immediately adjacent to the 5' DNA nucleoside of region G. The 3' most nucleoside of region F is a sugar modified nucleoside, such as a high affinity sugar modified nucleoside, for example a 2' substituted nucleoside, such as a MOE nucleoside, or an LNA nucleoside.

15 Region F' is positioned immediately adjacent to the 3' DNA nucleoside of region G. The 5' most nucleoside of region F' is a sugar modified nucleoside, such as a high affinity sugar modified nucleoside, for example a 2' substituted nucleoside, such as a MOE nucleoside, or an LNA nucleoside.

20 Region F is 1-8 contiguous nucleotides in length, such as 2-6, such as 3-4 contiguous nucleotides in length. Advantageously the 5' most nucleoside of region F is a sugar modified nucleoside. In some embodiments the two 5' most nucleoside of region F are sugar modified nucleoside. In some embodiments the 5' most nucleoside of region F is an LNA nucleoside. In some embodiments the two 5' most nucleoside of region F are LNA nucleosides. In some embodiments the two 5' most nucleoside of region F are 2' substituted nucleoside nucleosides, such as two 3' MOE nucleosides. In some
25 embodiments the 5' most nucleoside of region F is a 2' substituted nucleoside, such as a MOE nucleoside.

30 Region F' is 2-8 contiguous nucleotides in length, such as 3-6, such as 4-5 contiguous nucleotides in length. Advantageously, embodiments the 3' most nucleoside of region F' is a sugar modified nucleoside. In some embodiments the two 3' most nucleoside of region F' are sugar modified nucleoside. In some embodiments the two 3' most nucleoside of region F' are LNA nucleosides. In some embodiments the 3' most nucleoside of region F' is an LNA nucleoside. In some embodiments the two 3' most nucleoside of region F' are 2' substituted nucleoside nucleosides, such as two 3' MOE nucleosides. In some embodiments the 3' most nucleoside of region F' is a 2' substituted
35 nucleoside, such as a MOE nucleoside.

It should be noted that when the length of region F or F' is one, it is advantageously an LNA nucleoside.

In some embodiments, region F and F' independently consists of or comprises a contiguous sequence of sugar modified nucleosides. In some embodiments, the sugar
5 modified nucleosides of region F may be independently selected from 2'-O-alkyl-RNA units, 2'-O-methyl-RNA, 2'-amino-DNA units, 2'-fluoro-DNA units, 2'-alkoxy-RNA, MOE units, LNA units, arabino nucleic acid (ANA) units and 2'-fluoro-ANA units.

In some embodiments, region F and F' independently comprises both LNA and a 2' substituted modified nucleosides (mixed wing design).

10 In some embodiments, region F and F' consists of only one type of sugar modified nucleosides, such as only MOE or only beta-D-oxy LNA or only ScET. Such designs are also termed uniform flanks or uniform gapmer design.

In some embodiments, all the nucleosides of region F or F', or F and F' are LNA nucleosides, such as independently selected from beta-D-oxy LNA, ENA or ScET
15 nucleosides. In some embodiments region F consists of 1-5, such as 2-4, such as 3-4 such as 1, 2, 3, 4 or 5 contiguous LNA nucleosides. In some embodiments, all the nucleosides of region F and F' are beta-D-oxy LNA nucleosides.

In some embodiments, all the nucleosides of region F or F', or F and F' are 2' substituted nucleosides, such as OMe or MOE nucleosides. In some embodiments region F
20 consists of 1, 2, 3, 4, 5, 6, 7, or 8 contiguous OMe or MOE nucleosides. In some embodiments only one of the flanking regions can consist of 2' substituted nucleosides, such as OMe or MOE nucleosides. In some embodiments it is the 5' (F) flanking region that consists 2' substituted nucleosides, such as OMe or MOE nucleosides whereas the 3' (F') flanking region comprises at least one LNA nucleoside, such as beta-D-oxy LNA
25 nucleosides or cET nucleosides. In some embodiments it is the 3' (F') flanking region that consists 2' substituted nucleosides, such as OMe or MOE nucleosides whereas the 5' (F) flanking region comprises at least one LNA nucleoside, such as beta-D-oxy LNA nucleosides or cET nucleosides.

In some embodiments, all the modified nucleosides of region F and F' are LNA
30 nucleosides, such as independently selected from beta-D-oxy LNA, ENA or ScET nucleosides, wherein region F or F', or F and F' may optionally comprise DNA nucleosides (an alternating flank, see definition of these for more details). In some embodiments, all the modified nucleosides of region F and F' are beta-D-oxy LNA nucleosides, wherein region F or F', or F and F' may optionally comprise DNA
35 nucleosides (an alternating flank, see definition of these for more details).

In some embodiments the 5' most and the 3' most nucleosides of region F and F' are LNA nucleosides, such as beta-D-oxy LNA nucleosides or ScET nucleosides.

In some embodiments, the internucleoside linkage between region F and region G is a phosphorothioate internucleoside linkage. In some embodiments, the internucleoside linkage between region F' and region G is a phosphorothioate internucleoside linkage. In some embodiments, the internucleoside linkages between the nucleosides of region F or F', F and F' are phosphorothioate internucleoside linkages.

Further gapmer designs are disclosed in WO 2004/046160, WO 2007/146511 and WO 2008/113832, hereby incorporated by reference.

10 ***LNA Gapmer***

An LNA gapmer is a gapmer wherein either one or both of region F and F' comprises or consists of LNA nucleosides. A beta-D-oxy gapmer is a gapmer wherein either one or both of region F and F' comprises or consists of beta-D-oxy LNA nucleosides.

15 In some embodiments the LNA gapmer is of formula: [LNA]₁₋₅-[region G]-[LNA]₁₋₅, wherein region G is as defined in the Gapmer region G definition.

MOE Gapmers

A MOE gapmers is a gapmer wherein regions F and F' consist of MOE nucleosides. In some embodiments the MOE gapmer is of design [MOE]₁₋₈-[Region G]-[MOE]₁₋₈, such as [MOE]₂₋₇-[Region G]₅₋₁₆-[MOE]₂₋₇, such as [MOE]₃₋₆-[Region G]-[MOE]₃₋₆, wherein region G is as defined in the Gapmer definition. MOE gapmers with a 5-10-5 design (MOE-DNA-MOE) have been widely used in the art.

Mixed Wing Gapmer

A mixed wing gapmer is an LNA gapmer wherein one or both of region F and F' comprise a 2' substituted nucleoside, such as a 2' substituted nucleoside independently selected from the group consisting of 2'-O-alkyl-RNA units, 2'-O-methyl-RNA, 2'-amino-DNA units, 2'-fluoro-DNA units, 2'-alkoxy-RNA, MOE units, arabino nucleic acid (ANA) units and 2'-fluoro-ANA units, such as a MOE nucleosides. In some embodiments wherein at least one of region F and F', or both region F and F' comprise at least one LNA nucleoside, the remaining nucleosides of region F and F' are independently selected from the group consisting of MOE and LNA. In some embodiments wherein at least one of region F and F', or both region F and F' comprise at least two LNA nucleosides, the remaining nucleosides of region F and F' are independently selected from the group

consisting of MOE and LNA. In some mixed wing embodiments, one or both of region F and F' may further comprise one or more DNA nucleosides.

Mixed wing gapmer designs are disclosed in WO 2008/049085 and WO 2012/109395, both of which are hereby incorporated by reference.

5 *Alternating Flank Gapmers*

Flanking regions may comprise both LNA and DNA nucleoside and are referred to as "alternating flanks" as they comprise an alternating motif of LNA-DNA-LNA nucleosides. Gapmers comprising such alternating flanks are referred to as "alternating flank gapmers". "Alternative flank gapmers" are thus LNA gapmer oligonucleotides where
 10 at least one of the flanks (F or F') comprises DNA in addition to the LNA nucleoside(s). In some embodiments at least one of region F or F', or both region F and F', comprise both LNA nucleosides and DNA nucleosides. In such embodiments, the flanking region F or F', or both F and F' comprise at least three nucleosides, wherein the 5' and 3' most nucleosides of the F and/or F' region are LNA nucleosides.

15 Alternating flank LNA gapmers are disclosed in WO 2016/127002.

An alternating flank region may comprise up to 3 contiguous DNA nucleosides, such as 1 to 2 or 1 or 2 or 3 contiguous DNA nucleosides.

The alternating flank can be annotated as a series of integers, representing a number of LNA nucleosides (L) followed by a number of DNA nucleosides (D), for example

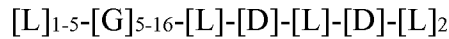
20 [L]₁₋₃-[D]₁₋₄-[L]₁₋₃

[L]₁₋₂-[D]₁₋₂-[L]₁₋₂-[D]₁₋₂-[L]₁₋₂

In oligonucleotide designs these will often be represented as numbers such that 2-2-1 represents 5' [L]₂-[D]₂-[L]₁ 3', and 1-1-1-1-1 represents 5' [L]-[D]-[L]-[D]-[L] 3'. The length of the flank (region F and F') in oligonucleotides with alternating flanks may
 25 independently be 3 to 10 nucleosides, such as 4 to 8, such as 5 to 6 nucleosides, such as 4, 5, 6 or 7 modified nucleosides. In some embodiments only one of the flanks in the gapmer oligonucleotide is alternating while the other is constituted of LNA nucleotides. It may be advantageous to have at least two LNA nucleosides at the 3' end of the 3' flank (F'), to confer additional exonuclease resistance. Some examples of oligonucleotides with
 30 alternating flanks are:

[L]₁₋₅-[D]₁₋₄-[L]₁₋₃-[G]₅₋₁₆-[L]₂₋₆

[L]₁₋₂-[D]₁₋₂-[L]₁₋₂-[D]₁₋₂-[L]₁₋₂-[G]₅₋₁₆-[L]₁₋₂-[D]₁₋₃-[L]₂₋₄



with the proviso that the overall length of the gapmer is at least 12, such as at least 14 nucleotides in length.

Region D' or D'' in an oligonucleotide

5 The oligonucleotide of the invention may in some embodiments comprise or consist of the contiguous nucleotide sequence of the oligonucleotide which is complementary to the target nucleic acid, such as the gapmer F-G-F', and further 5' and/or 3' nucleosides. The further 5' and/or 3' nucleosides may or may not be fully complementary to the target nucleic acid. Such further 5' and/or 3' nucleosides may be referred to as region D' and D''
10 herein.

The addition of region D' or D'' may be used for the purpose of joining the contiguous nucleotide sequence, such as the gapmer, to a conjugate moiety or another functional group. When used for joining the contiguous nucleotide sequence with a conjugate moiety it can serve as a bioleavable linker. Alternatively it may be used to
15 provide exonuclease protection or for ease of synthesis or manufacture.

Region D' and D'' can be attached to the 5' end of region F or the 3' end of region F', respectively to generate designs of the following formulas D'-F-G-F', F-G-F'-D'' or

D'-F-G-F'-D''. In this instance the F-G-F' is the gapmer portion of the oligonucleotide and region D' or D'' constitute a separate part of the oligonucleotide.

20 Region D' or D'' may independently comprise or consist of 1, 2, 3, 4 or 5 additional nucleotides, which may be complementary or non-complementary to the target nucleic acid. The nucleotide adjacent to the F or F' region is not a sugar-modified nucleotide, such as a DNA or RNA or base modified versions of these. The D' or D'' region may serve as a nuclease susceptible bioleavable linker (see definition of linkers). In some embodiments
25 the additional 5' and/or 3' end nucleotides are linked with phosphodiester linkages, and are DNA or RNA. Nucleotide based bioleavable linkers suitable for use as region D' or D'' are disclosed in WO 2014/076195, which include by way of example a phosphodiester linked DNA dinucleotide. The use of bioleavable linkers in poly-oligonucleotide constructs is disclosed in WO 2015/113922, where they are used to link multiple antisense
30 constructs (e.g. gapmer regions) within a single oligonucleotide.

In one embodiment the oligonucleotide of the invention comprises a region D' and/or D'' in addition to the contiguous nucleotide sequence which constitutes the gapmer.

In some embodiments, the oligonucleotide of the present invention can be represented by the following formulae:

F-G-F'; in particular F₁₋₈-G₅₋₁₆-F'₂₋₈

D'-F-G-F', in particular D'₁₋₃-F₁₋₈-G₅₋₁₆-F'₂₋₈

5 F-G-F'-D'', in particular F₁₋₈-G₅₋₁₆-F'₂₋₈-D''₁₋₃

D'-F-G-F'-D'', in particular D'₁₋₃-F₁₋₈-G₅₋₁₆-F'₂₋₈-D''₁₋₃

In some embodiments the internucleoside linkage positioned between region D' and region F is a phosphodiester linkage. In some embodiments the internucleoside linkage positioned between region F' and region D'' is a phosphodiester linkage.

10 **Totalmers**

In some embodiments, all of the nucleosides of the oligonucleotide, or contiguous nucleotide sequence thereof, are sugar modified nucleosides. Such oligonucleotides are referred to as a totalmers herein.

In some embodiments all of the sugar modified nucleosides of a totalmer comprise
 15 the same sugar modification, for example they may all be LNA nucleosides, or may all be 2'-O-MOE nucleosides. In some embodiments the sugar modified nucleosides of a totalmer may be independently selected from LNA nucleosides and 2' substituted nucleosides, such as 2' substituted nucleoside selected from the group consisting of 2'-O-alkyl-RNA, 2'-O-methyl-RNA, 2'-alkoxy-RNA, 2'-O-methoxyethyl-RNA (MOE), 2'-amino-DNA, 2'-
 20 Fluoro-RNA, and 2'-F-ANA nucleosides. In some embodiments the oligonucleotide comprises both LNA nucleosides and 2' substituted nucleosides, such as 2' substituted nucleoside selected from the group consisting of 2'-O-alkyl-RNA, 2'-O-methyl-RNA, 2'-alkoxy-RNA, 2'-O-methoxyethyl-RNA (MOE), 2'-amino-DNA, 2'-Fluoro-RNA, and 2'-F-ANA nucleosides. In some embodiments, the oligonucleotide comprises LNA
 25 nucleosides and 2'-O-MOE nucleosides. In some embodiments, the oligonucleotide comprises (S)cET LNA nucleosides and 2'-O-MOE nucleosides. In some embodiments, each nucleoside unit of the oligonucleotide is a 2'substituted nucleoside. In some embodiments, each nucleoside unit of the oligonucleotide is a 2'-O-MOE nucleoside.

In some embodiments, all of the nucleosides of the oligonucleotide or contiguous
 30 nucleotide sequence thereof are LNA nucleosides, such as beta-D-oxy-LNA nucleosides and/or (S)cET nucleosides. In some embodiments such LNA totalmer oligonucleotides are between 7 – 12 nucleosides in length (see for example, WO 2009/043353). Such short fully LNA oligonucleotides are particularly effective in inhibiting microRNAs.

Various totalmer compounds are highly effective as therapeutic oligomers, particularly when targeting microRNA (antimiRs) or as splice switching oligomers (SSOs).

In some embodiments, the totalmer comprises or consists of at least one **5** YXY sequence motif, such as a repeated sequence YXY or YXY, wherein X is LNA and Y is an alternative (i.e. non LNA) nucleotide analogue, such as a 2'-OMe RNA unit and 2'-fluoro DNA unit. The above sequence motif may, in some embodiments, be XXY, YXY, YXY or YXY for example.

In some embodiments, the totalmer may comprise or consist of a contiguous **10** nucleotide sequence of between 7 and 24 nucleotides, such as 7, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22 or 23 nucleotides.

In some embodiments, the contiguous nucleotide sequence of the totalmer comprises of at least 30%, such as at least 40%, such as at least 50%, such as at least 60%, such as at least 70%, such as at least 80%, such as at least 90%, such as 95%, such as 100% LNA **15** units. For full LNA compounds, it is advantageous that they are less than 12 nucleotides in length, such as 7 – 10.

The remaining units may be selected from the non-LNA nucleotide analogues referred to herein in, such those selected from the group consisting of 2'-O-alkyl-RNA unit, 2'-OMe-RNA unit, 2'-amino-DNA unit, 2'-fluoro-DNA unit, LNA unit, PNA unit, **20** HNA unit, INA unit, and a 2'MOE RNA unit, or the group 2'-OMe RNA unit and 2'-fluoro DNA unit.

Mixmers

The term 'mixmer' refers to oligomers which comprise both DNA nucleosides and sugar modified nucleosides, wherein there are insufficient length of contiguous DNA **25** nucleosides to recruit RNaseH. Suitable mixmers may comprise up to 3 or up to 4 contiguous DNA nucleosides. In some embodiments the mixmers, or contiguous nucleotide sequence thereof, comprise alternating regions of sugar modified nucleosides, and DNA nucleosides. By alternating regions of sugar modified nucleosides which form a RNA like (3'endo) conformation when incorporated into the oligonucleotide, with short **30** regions of DNA nucleosides, non-RNaseH recruiting oligonucleotides may be made. Advantageously, the sugar modified nucleosides are affinity enhancing sugar modified nucleosides.

Oligonucleotide mixmers are often used to provide occupation based modulation of target genes, such as splice modulators or microRNA inhibitors.

In some embodiments the sugar modified nucleosides in the mixmer, or contiguous nucleotide sequence thereof, comprise or are all LNA nucleosides, such as (S)cET or beta-D-oxy LNA nucleosides.

In some embodiments all of the sugar modified nucleosides of a mixmer comprise the same sugar modification, for example they may all be LNA nucleosides, or may all be 2'-O-MOE nucleosides. In some embodiments the sugar modified nucleosides of a mixmer may be independently selected from LNA nucleosides and 2' substituted nucleosides, such as 2' substituted nucleoside selected from the group consisting of 2'-O-alkyl-RNA, 2'-O-methyl-RNA, 2'-alkoxy-RNA, 2'-O-methoxyethyl-RNA (MOE), 2'-amino-DNA, 2'-Fluoro-RNA, and 2'-F-ANA nucleosides. In some embodiments the oligonucleotide comprises both LNA nucleosides and 2' substituted nucleosides, such as 2' substituted nucleoside selected from the group consisting of 2'-O-alkyl-RNA, 2'-O-methyl-RNA, 2'-alkoxy-RNA, 2'-O-methoxyethyl-RNA (MOE), 2'-amino-DNA, 2'-Fluoro-RNA, and 2'-F-ANA nucleosides. In some embodiments, the oligonucleotide comprises LNA nucleosides and 2'-O-MOE nucleosides. In some embodiments, the oligonucleotide comprises (S)cET LNA nucleosides and 2'-O-MOE nucleosides.

In some embodiments the mixmer, or contiguous nucleotide sequence thereof, comprises only LNA and DNA nucleosides, such LNA mixmer oligonucleotides which may for example be between 8 – 24 nucleosides in length (see for example, WO2007112754, which discloses LNA antmiR inhibitors of microRNAs).

Various mixmer compounds are highly effective as therapeutic oligomers, particularly when targeting microRNA (antimiRs) or as splice switching oligomers (SSOs).

In some embodiments, the mixmer comprises a motif

...[L]m[D]n[L]m[D]n[L]m... or

...[L]m[D]n[L]m[D]n[L]m[D]n[L]m ...or

...[L]m[D]n[L]m[D]n[L]m[D]n[L]m[D]n[L]m ... or

...[L]m[D]n[L]m[D]n[L]m[D]n[L]m[D]n[L]m[D]n[L]m ...

... [L]m[D]n[L]m[D]n[L]m[D]n[L]m[D]n[L]m[D]n[L]m[D]n[L]m... or

... [L]m[D]n[L]m[D]n[L]m[D]n[L]m[D]n[L]m[D]n[L]m[D]n[L]m ... or

... [L]m[D]n[L]m[D]n[L]m[D]n[L]m[D]n[L]m[D]n[L]m[D]n[L]m[D]n[L]m ... or

In some embodiments, the mixmer comprises at least a region comprising at least three consecutive nucleotide analogue units, such as at least three consecutive LNA units.

Exosomes

Exosomes are natural biological nanovesicles, typically in the range of 30 to 500 nm, that are involved in cell-cell communication via the functionally-active cargo (such as miRNA, mRNA, DNA and proteins).

Exosomes are secreted by all types of cells and are also found abundantly in the body fluids such as: saliva, blood, urine and milk. The major role of exosomes is to carry the information by delivering various effectors or signaling molecules between specific cells (Acta Pol Pharm. 2014 Jul-Aug;71(4):537-43.). Such effectors or signaling molecules can for example be proteins, miRNAs or mRNAs. Exosomes are currently being explored as a delivery vehicle for various drug molecules including RNA therapeutic molecules, to expand the therapeutic and diagnostic applications of such molecules. There are disclosures in the art of exosomes loaded with synthetic molecules such as siRNA, antisense oligonucleotides and small molecules which suggest or show advantages in terms of delivery and efficacy of such molecules compared to the free drug molecules (see for example Andaloussi et al 2013 Advanced Drug Delivery Reviews 65: 391-397, WO2014/168548, WO2016/172598, WO2017/173034 and WO 2018/102397).

Exosomes may be isolated from biological sources, such as milk (milk exosomes), in particular bovine milk is an abundant source for isolating bovine milk exosomes. See for example Manca et al., Scientific Reports (2018) 8:11321.

In some embodiments of the invention, the single stranded oligonucleotide is encapsulated in an exosome (exosome formulation), examples of loading an exosome with a single stranded antisense oligonucleotide are described in EP application No. 18192614.8. In the methods of the invention the antisense oligonucleotide may be administered to the cell or to the subject in the form of an exosome formulation, in particular oral administration of the exosome formulations are envisioned.

In some embodiments, the antisense oligonucleotide may be conjugated, e.g. with a lipophilic conjugate such as cholesterol, which may be covalently attached to the antisense oligonucleotide via a biocleavable linker (e.g. a region of phosphodiester linked DNA nucleotides). Such lipophilic conjugates can facilitate formulation of antisense oligonucleotides into exosomes and may further enhance the delivery to the target cell.

Conjugate

The term conjugate as used herein refers to an oligonucleotide which is covalently linked to a non-nucleotide moiety (conjugate moiety or region C or third region).

Conjugation of the oligonucleotide of the invention to one or more non-nucleotide moieties may improve the pharmacology of the oligonucleotide, *e.g.* by affecting the activity, cellular distribution, cellular uptake or stability of the oligonucleotide. In some embodiments the conjugate moiety modifies or enhance the pharmacokinetic properties of the oligonucleotide by improving cellular distribution, bioavailability, metabolism, excretion, permeability, and/or cellular uptake of the oligonucleotide. In particular, the conjugate may target the oligonucleotide to a specific organ, tissue or cell type and thereby enhance the effectiveness of the oligonucleotide in that organ, tissue or cell type. At the same time the conjugate may serve to reduce activity of the oligonucleotide in non-target cell types, tissues or organs, *e.g.* off target activity or activity in non-target cell types, tissues or organs.

WO 93/07883 and WO 2013/033230 provides suitable conjugate moieties, which are hereby incorporated by reference. Further suitable conjugate moieties are those capable of binding to the asialoglycoprotein receptor (ASGPR). In particular, tri-valent N-acetylgalactosamine conjugate moieties are suitable for binding to the ASGPR, see for example WO 2014/076196, WO 2014/207232 and WO 2014/179620 (hereby incorporated by reference). Such conjugates serve to enhance uptake of the oligonucleotide to the liver while reducing its presence in the kidney, thereby increasing the liver/kidney ratio of a conjugated oligonucleotide compared to the unconjugated version of the same oligonucleotide.

Oligonucleotide conjugates and their synthesis has also been reported in comprehensive reviews by Manoharan in *Antisense Drug Technology, Principles, Strategies, and Applications*, S.T. Crooke, ed., Ch. 16, Marcel Dekker, Inc., 2001 and Manoharan, *Antisense and Nucleic Acid Drug Development*, 2002, 12, 103, each of which is incorporated herein by reference in its entirety.

In an embodiment, the non-nucleotide moiety (conjugate moiety) is selected from the group consisting of carbohydrates, cell surface receptor ligands, drug substances, hormones, lipophilic substances, polymers, proteins, peptides, toxins (*e.g.* bacterial toxins), vitamins, viral proteins (*e.g.* capsids) or combinations thereof.

Linkers

A linkage or linker is a connection between two atoms that links one chemical group or segment of interest to another chemical group or segment of interest via one or more covalent bonds. Conjugate moieties can be attached to the oligonucleotide directly or

through a linking moiety (e.g. linker or tether). Linkers serve to covalently connect a third region, e.g. a conjugate moiety (Region C), to a first region, e.g. an oligonucleotide or contiguous nucleotide sequence complementary to the target nucleic acid (region A).

5 In some embodiments of the invention the conjugate or oligonucleotide conjugate of the invention may optionally, comprise a linker region (second region or region B and/or region Y) which is positioned between the oligonucleotide or contiguous nucleotide sequence complementary to the target nucleic acid (region A or first region) and the conjugate moiety (region C or third region).

10 Region B refers to biocleavable linkers comprising or consisting of a physiologically labile bond that is cleavable under conditions normally encountered or analogous to those encountered within a mammalian body. Conditions under which physiologically labile linkers undergo chemical transformation (e.g., cleavage) include chemical conditions such as pH, temperature, oxidative or reductive conditions or agents, and salt concentration found in or analogous to those encountered in mammalian cells. Mammalian intracellular
15 conditions also include the presence of enzymatic activity normally present in a mammalian cell such as from proteolytic enzymes or hydrolytic enzymes or nucleases. In one embodiment the biocleavable linker is susceptible to S1 nuclease cleavage. In a preferred embodiment the nuclease susceptible linker comprises between 1 and 10 nucleosides, such as 1, 2, 3, 4, 5, 6, 7, 8, 9 or 10 nucleosides, more preferably between 2
20 and 6 nucleosides and most preferably between 2 and 4 linked nucleosides comprising at least two consecutive phosphodiester linkages, such as at least 3 or 4 or 5 consecutive phosphodiester linkages. Preferably the nucleosides are DNA or RNA. Phosphodiester containing biocleavable linkers are described in more detail in WO 2014/076195 (hereby incorporated by reference).

25 Region Y refers to linkers that are not necessarily biocleavable but primarily serve to covalently connect a conjugate moiety (region C or third region), to an oligonucleotide (region A or first region). The region Y linkers may comprise a chain structure or an oligomer of repeating units such as ethylene glycol, amino acid units or amino alkyl groups. The oligonucleotide conjugates of the present invention can be constructed of the
30 following regional elements A-C, A-B-C, A-B-Y-C, A-Y-B-C or A-Y-C. In some embodiments the linker (region Y) is an amino alkyl, such as a C2 – C36 amino alkyl group, including, for example C6 to C12 amino alkyl groups. In a preferred embodiment the linker (region Y) is a C6 amino alkyl group.

Administration

35 The oligonucleotides or pharmaceutical compositions of the present invention may be administered topical (such as, to the skin, inhalation, ophthalmic or otic) or enteral

(such as, orally or through the gastrointestinal tract) or parenteral (such as, intravenous, subcutaneous, intra-muscular, intracerebral, intracerebroventricular or intrathecal).

In some embodiments the oligonucleotide or pharmaceutical compositions of the present invention are administered by a parenteral route including intravenous,
5 intraarterial, subcutaneous, intraperitoneal or intramuscular injection or infusion, intrathecal or intracranial, e.g. intracerebral or intraventricular, intravitreal administration. In one embodiment the active oligonucleotide or oligonucleotide conjugate is administered intravenously. In another embodiment the active oligonucleotide or oligonucleotide conjugate is administered subcutaneously.

10 In some embodiments, the oligonucleotide, oligonucleotide conjugate or pharmaceutical composition of the invention is administered at a dose of 0.1 – 15 mg/kg, such as from 0.2 – 10 mg/kg, such as from 0.25 – 5 mg/kg. The administration can be once a week, every 2nd week, every third week or once a month or bi monthly.

The invention also provides for the use of the oligonucleotide or oligonucleotide
15 conjugate of the invention as described for the manufacture of a medicament wherein the medicament is in a dosage form for ophthalmic such as intravitreal injection. In some embodiments, the oligonucleotide for ophthalmic targets is Htra-1.

The invention also provides for the use of the oligonucleotide or oligonucleotide conjugate of the invention as described for the manufacture of a medicament wherein the
20 medicament is in a dosage form for intravenous, subcutaneous, intra-muscular, intracerebral, intracerebroventricular or intrathecal administration (e.g. injection).

Illustrative Advantages

As illustrated herein the achiral phosphorodithioate internucleoside linkage used in the compounds of invention allows for the reduction of the complexity of a non-
25 stereodefined phosphorothioate oligonucleotide, whilst maintaining the activity, efficacy or potency of the oligonucleotide.

Indeed, as illustrated herein, the used in the compounds of invention provides unique benefits in combination with stereodefined phosphorothioates, providing the opportunity to further reduce the complexity of phosphorothioate oligonucleotides, whilst retaining or
30 improving the activity, efficacy or potency of the oligonucleotide.

As illustrated herein the achiral phosphorodithioate internucleoside linkage used in the compounds of invention allows for improvement in cellular uptake in vitro or in vivo.

As illustrated herein the achiral phosphorodithioate internucleoside linkage used in the compounds of invention allows for alteration or improvement in biodistribution in vitro (measured either as tissue or cell content, or activity/potency in target tissues). Notably we have seen improvement of tissue uptake, content and /or potency in skeletal muscle, heart, spleen, liver, kidney, fibroblasts, epithelial cells.

In the context of a mixmer oligonucleotides, the inventors have identified incorporating a phosphorodithioate linkages (as shown in IA or IB), between or adjacent to one or more DNA nucleosides, provides improvements, such as enhanced stability and/or improved potency. In the context of gapmer oligonucleotides the inventors has seen that incorporation of phosphorodithioate linkages (as shown in IA or IB) between the nucleosides of the flank region (such as between 2'sugar modified nucleosides) also provides improvements, such as enhanced stability and/or improved potency.

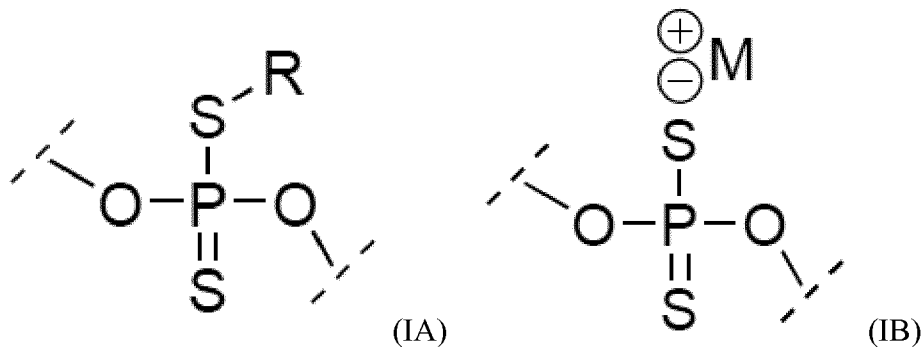
As illustrated herein the achiral phosphorodithioate internucleoside linkage used in the compounds of invention allows for improvement in oligonucleotide stability. The incorporation of the achiral phosphorodithioate internucleoside in the compounds of the invention provides enhanced resistance to serum and cellular exonucleases, particularly 3' exonucleases, but also 5' exonucleases, and the remarkable stability of the compounds of the invention further indicate a resistance to endonucleases for compounds which incorporate the achiral phosphorodithioate linkages. The stabilization of oligonucleotides is of particular importance in reducing or preventing the accumulation of toxic degradation products, and prolonging the duration of action of the antisense oligonucleotide. As illustrated in the examples rat serum stability may be used to assay for improved stability. For evaluation of cellular stability, tissue (e.g. liver) homogenate extract may be used – for example see WO2014076195 which provided such methods). Other assays for measuring oligonucleotide stability include snake venom phosphodiesterase stability assays and S1 nuclease stability).

Reduced toxicity risk of the claimed oligonucleotides is tested in vitro hepatotoxicity assays (e.g. as disclosed in WO 2017/067970) or in vitro nephrotoxicity assays (e.g. as disclosed in WO 2017/216340), or in vitro neurotoxicity assays (e.g. as disclosed in WO2016127000). Alternatively, toxicity may be assayed in vivo, for example in mouse or rat.

Enhanced stability can provide benefits to the duration of action of the oligonucleotides of the invention, which is of particular benefit for when the administration route is invasive, e.g. parenteral administration, such as, intravenous, subcutaneous, intra-muscular, intracerebral, intraocular, intracerebroventricular or intrathecal administration.

GAPMER EMBODIMENTS

1. An antisense gapmer oligonucleotide, for inhibition of a target RNA in a cell, wherein the antisense gapmer oligonucleotide comprises at least one phosphorodithioate internucleoside linkage of formula (IA) or (IB)



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wherein in (IA) R is hydrogen or a phosphate protecting group, and in (IB) M⁺ is a cation, such as a metal cation, such as an alkali metal cation, such as a Na⁺ or K⁺ cation; or M⁺ is an ammonium cation.

2. The antisense gapmer oligonucleotide according to embodiment 1, wherein the at least one phosphorodithioate internucleoside linkage is of formula (IA), and R is hydrogen; or the at least one phosphorodithioate internucleoside linkage is of formula (IB), and M⁺ is Na⁺, K⁺ or ammonium.
3. A gapmer oligonucleotide according to embodiment 1 or 2, wherein one of the two oxygen atoms of said at least one internucleoside linkage of formula (I) is linked to the 3' carbon atom of an adjacent nucleoside (A¹) and the other one is linked to the 5' carbon atom of another nucleoside (A²), wherein at least one of the two nucleosides (A¹) and (A²) is a 2'-sugar modified nucleoside.
4. A gapmer oligonucleotide according to any one of embodiments 1 - 3, wherein one of (A¹) and (A²) is a 2'-sugar modified nucleoside and the other one is a DNA nucleoside.
5. A gapmer oligonucleotide according to any one of embodiments 1 - 3, wherein (A¹) and (A²) are both a 2'-modified nucleoside at the same time.
6. A gapmer oligonucleotide according to any one of embodiments 1 - 3, wherein (A¹) and (A²) are both a DNA nucleoside at the same time.

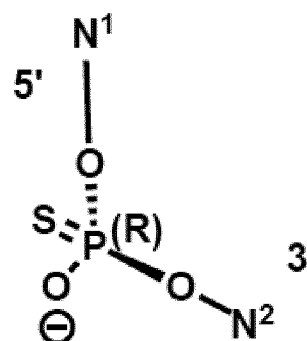
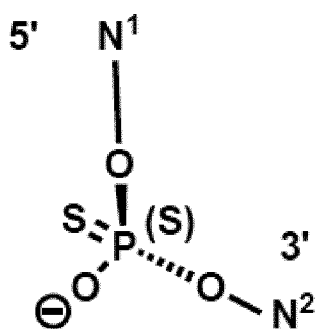
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7. A gapmer oligonucleotide according to any one of embodiments 1 to 6, wherein the gapmer oligonucleotide comprises a contiguous nucleotide sequence of formula 5'-F-G-F'-3', wherein G is a region of 5 to 18 nucleosides which is capable of recruiting RNaseH, and said region G is flanked 5' and 3' by flanking regions F and F' respectively, wherein regions F and F' independently comprise or consist of 1 to 7 2'-sugar modified nucleotides, wherein the nucleoside of region F which is adjacent to region G is a 2'-sugar modified nucleoside and wherein the nucleoside of region F' which is adjacent to region G is a 2'-sugar modified nucleoside.
8. A gapmer oligonucleotide according to any one of embodiments 1 to 7, wherein the 2'-sugar modified nucleosides are independently selected from 2'-alkoxy-RNA, 2'-alkoxyalkoxy-RNA, 2'-amino-DNA, 2'-fluoro-RNA, 2'-fluoro-ANA and LNA nucleosides.
9. A gapmer oligonucleotide according to embodiment 8, wherein 2'-alkoxyalkoxy-RNA is a 2'-methoxyethoxy-RNA (2'-O-MOE).
10. A gapmer oligonucleotide according to any one of embodiments 7 to 8, wherein region F and region F' comprise or consist of 2'-methoxyethoxy-RNA nucleotides.
11. A gapmer oligonucleotide according to any one of embodiments 7 to 10, wherein at least one or all of the 2'-sugar modified nucleosides in region F or region F', or in both regions F and F', are LNA nucleosides.
12. A gapmer oligonucleotide according to any one of embodiments 7 to 11, wherein region F or region F', or both regions F and F', comprise at least one LNA nucleoside and at least one DNA nucleoside.
13. A gapmer oligonucleotide according to any one of embodiments 7 to 12, wherein region F or region F', or both region F and F' comprise at least one LNA nucleoside and at least one non-LNA 2'-sugar modified nucleoside, such as at least one 2'-methoxyethoxy-RNA nucleoside.
14. A gapmer oligonucleotide according to any one of embodiments 1 to 13, wherein the gap region comprises 5 to 16, in particular 8 to 16, more particularly 8, 9, 10, 11, 12, 13 or 14 contiguous DNA nucleosides.
15. A gapmer oligonucleotide according to any one of embodiments 1 to 14, wherein region F and region F' are independently 1, 2, 3, 4, 5, 6, 7 or 8 nucleosides in length.
16. A gapmer oligonucleotide according to any one of embodiments 1 to 15, wherein region F and region F' each independently comprise 1, 2, 3 or 4 LNA nucleosides.

17. A gapmer oligonucleotide according to any one of embodiments 8 to 16, wherein the LNA nucleosides are independently selected from beta-D-oxy LNA, 6'-methyl-beta-D-oxy LNA and ENA.
18. A gapmer oligonucleotide according to embodiments 8 - 18, wherein the LNA nucleosides are beta-D-oxy LNA.
19. A gapmer oligonucleotide according to any one of embodiments 1 to 18, wherein the oligonucleotide, or contiguous nucleotide sequence thereof (F-G-F'), is of 10 to 30 nucleotides in length, in particular 12 to 22, more particularly of 14 to 20 oligonucleotides in length.
20. The gapmer oligonucleotide according to any one of embodiments 1 - 19, wherein at least one of the flank regions, such as region F and F' comprise a phosphorodithioate linkage of formula (IA) or (IB), as defined in any one of embodiments 1 - 19.
21. The gapmer oligonucleotide according to any one of embodiments 1 - 19, wherein both flank regions, such as region F and F' comprise a phosphorodithioate linkage of formula (IA) or (IB), as defined in any one of embodiments 1 - 19.
22. The gapmer oligonucleotide according to any one of embodiments 1 - 21, wherein at least one of the flank regions, such as F or F' comprises at least two phosphorodithioate linkage of formula (IA) or (IB), as defined in any one of embodiments 1 - 19.
23. The gapmer oligonucleotide according to any one of embodiments 1 - 21, wherein both the flank regions, F and F' comprises at least two phosphorodithioate linkage of formula (IA) or (IB), as defined in any one of embodiments 1 - 19.
24. The gapmer oligonucleotide according to any one of embodiments 1 - 23, wherein the one or both of the flank regions each comprise a LNA nucleoside which has a phosphorodithioate linkage of formula (IA) or (IB) linking the LNA to a 3' nucleoside.
25. The gapmer oligonucleotide according to any one of embodiments 1 - 24, wherein one or both flank regions each comprise two or more adjacent LNA nucleosides which are linked by phosphorodithioate linkage of formula (IA) or (IB) linking the LNA to a 3' nucleoside.
26. The gapmer oligonucleotide according to any one of embodiments 1 - 25, wherein one or both flank regions each comprise a MOE nucleoside which has a

phosphorodithioate linkage of formula (IA) or (IB) linking the MOE to a 3' nucleoside.

27. The gapmer oligonucleotide according to any one of embodiments 1 – 26, wherein one or both flank regions each comprise two or more adjacent MOE nucleosides which are linked by phosphorodithioate linkage of formula (IA) or (IB) linking the MOE to a 3' nucleoside.
28. The gapmer oligonucleotide according to any one of embodiments 1 – 27, wherein the flank regions, F and F' together comprise 1, 2, 3, 4 or 5 phosphorodithioate internucleoside linkages for formula (IA) or (IB), and wherein optionally, the internucleoside linkage between the 3' most nucleoside of region F and the 5' most nucleoside of region G is also a phosphorodithioate internucleoside linkages for formula (IA) or (IB).
29. A gapmer oligonucleotide according to any one of embodiments 1 to 28, which comprises 1 a phosphorodithioate internucleoside linkage of formula (IA) or (IB) positioned between adjacent nucleosides in region F or region F', between region F and region G or between region G and region F'.
30. The gapmer region according to any one of embodiments 1 – 29, wherein the gap region comprises 1, 2, 3 or 4 phosphorodithioate internucleoside linkages for formula (IA) or (IB), wherein the remaining internucleoside linkages are phosphorothioate internucleoside linkages.
31. The gapmer according to any one of embodiments 1 – 30, where in the gap region comprises a region of at least 5 contiguous DNA nucleotides, such as a region of 6 – 18 DNA contiguous nucleotides, or 8 – 14 contiguous DNA nucleotides.
32. The gapmer according to any one of embodiments 1 – 31, which further comprises one or more stereodefined phosphorothioate internucleoside linkages (Sp, S) or (Rp, R)



wherein N¹ and N² are nucleosides.

33. The gapmer according to embodiment 32, wherein the gapmer comprises at least one stereodefined internucleoside linkage (Sp, S) or (Rp, R) between two DNA nucleosides, such as between two DNA nucleoside in the gap region.
- 5 34. The gapmer oligonucleotide according to embodiment 32 or 33, wherein the gap region comprises 2, 3, 4, 5, 6, 7 or 8 stereodefined phosphorothioate internucleoside linkages, independently selected from Rp and Sp internucleoside linkages.
35. The gapmer oligonucleotide according to any one of embodiments 32 - 33, wherein region G further comprises at least 2, 3, or 4 internucleoside linkages of formula IB.
- 10 34. The gapmer oligonucleotide according to embodiments 32 – 35, wherein either (i) all remaining internucleoside linkages within region G (i.e. between the nucleoside in region G) are either stereodefined phosphorothioate internucleoside linkages, independently selected from Rp and Sp internucleoside linkages, or (ii) all the internucleoside linkages within region G are either stereodefined phosphorothioate internucleoside linkages, independently selected from Rp and Sp internucleoside linkages.
- 15 35. The gapmer oligonucleotide according to any one of embodiments 1 – 34, wherein all the internucleoside linkages within the flank regions are phosphorodithioate internucleoside linkages of formula (IA) or (IB), wherein optionally the internucleoside linkage between the 3' most nucleoside of region F and the 5' most nucleoside of region G is also a phosphorodithioate internucleoside linkages for formula (IA) or (IB), and the internucleoside linkage between the 3' most nucleoside of region G and the 5' most nucleoside of region F' is a stereodefined phosphorothioate internucleoside linkage.
- 20 36. A gapmer oligonucleotide according to any one of embodiments 6 to 35, wherein the internucleoside linkages between the nucleosides of region G are independently selected from phosphorothioate internucleoside linkages and phosphorodithioate internucleoside linkages of formula (I) as defined in embodiment 1.
37. A gapmer oligonucleotide according to any one of embodiments 7 to 36 wherein the internucleoside linkages between the nucleosides of region G comprise 0, 1, 2 or 3 phosphorodithioate internucleoside linkages of formula (I) as defined in embodiment 1, in particular 0 phosphorodithioate internucleoside linkages of formula (I).
- 30 38. A gapmer oligonucleotide according to any one of embodiments 1 to 37, wherein the remaining internucleoside linkages are independently selected from the group

consisting of phosphorothioate, phosphodiester and phosphorodithioate internucleoside linkages of formula (I) as defined in embodiment 1.

39. A gapmer oligonucleotide according to any one of embodiments 7 to 38, wherein the internucleoside linkages between the nucleosides of region F and the internucleoside linkages between the nucleosides of region F' are independently selected from phosphorothioate and phosphorodithioate internucleoside linkages of formula (I) as defined in embodiment 1.
40. A gapmer oligonucleotide according to any one of embodiments 7 to 39, wherein each flanking region F and F' independently comprise 1, 2, 3, 4, 5, 6 or 7 phosphorodithioate internucleoside linkages of formula (I) as defined in embodiment 1.
41. A gapmer oligonucleotide according to any one of embodiments 7 to 40, wherein all the internucleoside linkages of flanking regions F and/or F' are phosphorodithioate internucleoside linkages of formula (I) as defined in embodiment 1.
42. A gapmer oligonucleotide according to any one of embodiments 1 to 41, wherein the gapmer oligonucleotide comprises at least one stereodefined internucleoside linkage, such as at least one stereodefined phosphorothioate internucleoside linkage.
43. A gapmer oligonucleotide according to any one of embodiments 1 to 42, wherein the gap region comprises 1, 2, 3, 4 or 5 stereodefined phosphorothioate internucleoside linkages.
44. A gapmer oligonucleotide according to any one of embodiments 1 to 43, wherein all the internucleoside linkages between the nucleosides of the gap region are stereodefined phosphorothioate internucleoside linkages.
45. A gapmer oligonucleotide according to any one of embodiments 7 to 44, wherein the at least one phosphorodithioate internucleoside linkage of formula (IA) or (IB) is positioned between the nucleosides of region F, or between the nucleosides of region F', or between region F and region G, or between region G and region F', and the remaining internucleoside linkages within region F and F', between region F and region G and between region G and region F', are independently selected from stereodefined phosphorothioate internucleoside linkages, stereorandom internucleoside linkages, phosphorodithioate internucleoside linkage of formula (IA) or (IB) and phosphodiester internucleoside linkages.
46. A gapmer oligonucleotide according to embodiment 45, wherein the remaining internucleoside linkages within region F, within region F' or within both region F

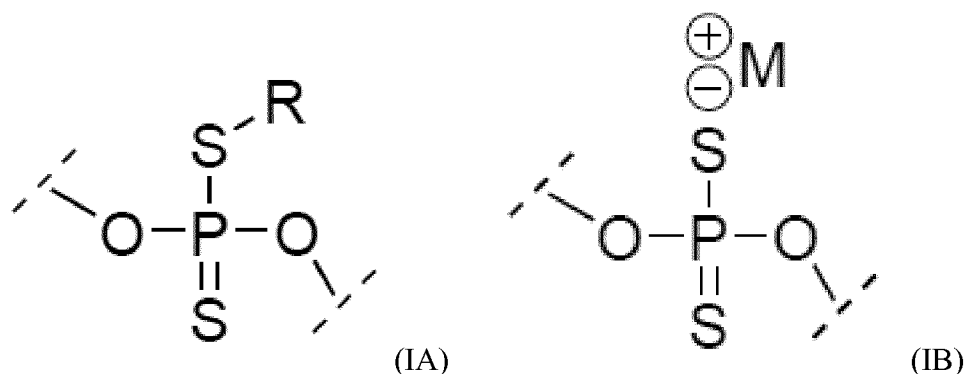
and region F' are all phosphorodithioate internucleoside linkages of formula (IA) or (IB).

47. A gapmer oligonucleotide according to any one of embodiments 6 to 33, wherein the internucleoside linkages between the nucleosides of gerion G comprise 0, 1, 2 or 3 phosphorodithioate internucleoside linkages of formula (I) as defined in embodiment 1 and the remaining internucleoside linkages within region G are independently selected from stereodefined phosphorothioate internucleoside linkages, stereorandom internucleoside linkages and phosphodiester internucleoside linkages.
48. The gapmer oligonucleotide according to any one of embodiments 1 - 47, wherein the 3' terminal nucleoside of the antisense oligonucleotide is a LNA nucleoside or a 2'-O-MOE nucleoside.
49. The gapmer oligonucleotide according to any one of embodiments 1 - 48, wherein the 5' terminal nucleoside of the antisense oligonucleotide is a LNA nucleoside or a 2'-O-MOE nucleoside.
50. The gapmer oligonucleotide according to any one of embodiments 1 - 49, wherein the two 3' most terminal nucleosides of the antisense oligonucleotide are independently selected from LNA nucleosides and 2'-O-MOE nucleosides.
51. The gapmer oligonucleotide according to any one of embodiments 1-50, wherein the two 5' most terminal nucleosides of the antisense oligonucleotide are independently selected from LNA nucleosides and 2'-O-MOE nucleosides.
52. The gapmer oligonucleotide according to any one of embodiments 1 - 51, wherein the three 3' most terminal nucleosides of the antisense oligonucleotide are independently selected from LNA nucleosides and 2'-O-MOE nucleosides.
53. The gapmer oligonucleotide according to any one of embodiments 1 - 52, wherein the three 5' most terminal nucleosides of the antisense oligonucleotide are independently selected from LNA nucleosides and 2'-O-MOE nucleosides.
54. The gapmer oligonucleotide according to any one of embodiments 1 - 53, wherein the two 3' most terminal nucleosides of the antisense oligonucleotide are LNA nucleosides.
55. The gamper oligonucleotide according to any one of embodiments 1 - 54, wherein the two 5' most terminal nucleosides of the antisense oligonucleotide are LNA nucleosides.

56. The gapmer oligonucleotide according to any one of embodiments 1 – 55, wherein nucleoside (A²) of formula (IA) or (IB) is the 3' terminal nucleoside of the oligonucleotide.
57. The gapmer oligonucleotide according to any one of embodiments 1 – 56, wherein nucleoside (A¹) of formula (IA) or (IB) is the 5' terminal nucleoside of the oligonucleotide.
58. The gapmer oligonucleotide according to any one of embodiments 7 – 57, wherein the gapmer oligonucleotide comprises a contiguous nucleotide sequence of formula 5'-D'-F-G-F'-D''-3', wherein F, G and F' are as defined in any one of embodiments 7 to 45 and wherein region D' and D'' each independently consist of 0 to 5 nucleotides, in particular 2, 3 or 4 nucleotides, in particular DNA nucleotides such as phosphodiester linked DNA nucleosides [an oligonucleotide which comprises the gapmer oligonucleotide, and a flanking sequence].
59. A gapmer oligonucleotide according to any one of embodiments 1 to 58, wherein the gapmer oligonucleotide is capable of recruiting human RNaseH1.
60. A gapmer oligonucleotide according to any one of embodiments 1 to 59, wherein the gapmer oligonucleotide is for the in vitro or in vivo inhibition of a mammalian, such as a human, mRNA or pre-mRNA target, or a viral target, or a long non coding RNA.
61. A pharmaceutically acceptable salt of a gapmer oligonucleotide according to any one of embodiments 1 to 60, in particular a sodium or a potassium salt.
62. A conjugate comprising a gapmer oligonucleotide or a pharmaceutically acceptable salt according to any one of embodiments 1 to 61 and at least one conjugate moiety covalently attached to said oligonucleotide or said pharmaceutically acceptable salt, optionally *via* a linker moiety.
63. A pharmaceutical composition comprising a gapmer oligonucleotide, pharmaceutically acceptable salt or conjugate according to any one of embodiments 1 to 62 and a therapeutically inert carrier.
64. A gapmer oligonucleotide, pharmaceutically acceptable salt or conjugate according to any one of embodiments 1 to 63 for use as a therapeutically active substance.

ANTISENSE OLIGONUCLEOTIDE EMBODIMENTS

The invention relates to an oligonucleotide comprising at least one phosphorodithioate internucleoside linkage of formula (IA) or (IB)



wherein one of the two oxygen atoms is linked to the 3' carbon atom of an adjacent nucleoside (A¹) and the other one is linked to the 5' carbon atom of another adjacent nucleoside (A²), and wherein in (IA) R is hydrogen or a phosphate protecting group, and
 5 in (IB) M⁺ is a cation, such as a metal cation, such as an alkali metal cation, such as a Na⁺ or K⁺ cation; or M⁺ is an ammonium cation.

Alternatively stated M is a metal, such as an alkali metal, such as Na or K; or M is NH₄.

The oligonucleotide may, for example, be a single stranded antisense oligonucleotide,
 10 which is capable of modulating the expression of a target nucleic acid, such as a target microRNA, or is capable of modulating the splicing of a target pre-mRNA, which comprises a contiguous nucleotide sequence. The antisense oligonucleotide of the invention comprises a contiguous nucleotide sequence which is complementary to the target nucleic acid, and is capable of hybridizing to and modulating the expression of the
 15 target nucleic acid. In a preferred embodiment, the antisense oligonucleotide, or the contiguous nucleotide sequence thereof, is a mixmer oligonucleotide wherein either (A¹) or (A²) is a DNA nucleoside, or both (A¹) and (A²) are DNA nucleosides.

In the context of the present invention an antisense oligonucleotide is a single stranded oligonucleotide which is complementary to a nucleic acid target, such as a target
 20 RNA, and is capable of modulating (e.g. splice modulating of a pre-mRNA target) or inhibiting the expression of the nucleic acid target (e.g. a mRNA target, a premRNA target, a viral RNA target, or a long non coding RNA target). Depending on the target the length of the oligonucleotide or the length of the region thereof which is complementary to (i.e. antisense – preferably the complementary region is fully complementary to the target) may
 25 be 7 – 30 nucleotides (the region which is referred to as the contiguous nucleotide sequence). For example LNA nucleotide inhibitors of microRNAs may be as short as 7 contiguous complementary nucleotides (and may be as long as 30 nucleotides), RNaseH recruiting oligonucleotides are typically at least 12 contiguous complementary nucleotides in length, such as 12- 26 nucleotides in length. Splice modulating antisense

oligonucleotides typically has a contiguous nucleotide region of 10 – 30 complementary nucleotides.

Splice modulating oligonucleotides, also known as splice-switching oligonucleotides (SSOs) are short, synthetic, antisense, modified nucleic acids that base-pair with a pre-mRNA and disrupt the normal splicing repertoire of the transcript by blocking the RNA–RNA base-pairing or protein–RNA binding interactions that occur between components of the splicing machinery and the pre-mRNA. Splicing of pre-mRNA is required for the proper expression of the vast majority of protein-coding genes, and thus, targeting the process offers a means to manipulate protein production from a gene. Splicing modulation is particularly valuable in cases of disease caused by mutations that lead to disruption of normal splicing or when interfering with the normal splicing process of a gene transcript may be therapeutic. SSOs offer an effective and specific way to target and alter splicing in a therapeutic manner. See Haven's and Hasting NAR (2016) 44, 6549-6563. SSOs may be complementary to an Exon/Intron boundary in the target pre-mRNA or may target splicing enhanced or silencer elements (collectively referred to as cis-acting splice elements) within the pre-mRNA that regulates splicing of the pre-mRNA. Splice modulation may result in exon skipping, or exon inclusion and thereby modulates alternative splicing of a pre-mRNA. SSOs function by non nuclease mediated modulation of the target pre-mRNA, and therefore are not capable of recruiting RNaseH, they are often either fully modified oligonucleotides, i.e. each nucleoside comprises a modified sugar moiety, such as a 2'sugar substituted sugar moiety (for example fully 2'-O-MOE oligonucleotides of e.g. 15 – 25 nucleotides in length, often 18 – 22 or 20 nucleotides in length, based on a phosphorothioate back bone), or LNA mixmer oligonucleotides (oligonucleotides 10 – 30 nucleotides in length which comprises DNA and LNA nucleosides, and optionally other 2' sugar modified nucleosides, such as 2'-O-MOE. Also envisaged are LNA oligonucleotides which do not comprises DNA nucleosides, but comprise of LNA and other 2' sugar modified nucleosides, such as 2'-O-MOE nucleosides. Table 1 of Haven's and Hasting NAR (2016) 44, 6549-6563, hereby incorporated by reference, illustrates a range of SSO targets and the chemistry of the oligonucleotides used which have reported activity in vivo, and is reproduced below in Table A:

TABLE A

Condition	Target gene	Stage/Mode I	SSO	Target (Action)	Route	Ref (see Haven's and Hasting)

Condition	Target gene	Stage/Model	SSO	Target (Action)	Route	Ref (see Haven's and Hastings)
Block cryptic/Aberrant splicing caused by mutations						
β -Thalassemia	<i>HBB</i>	mouse	PPMO	intron 2 aberrant 5'ss (correct splicing)	IV	(<u>144</u>)
Fukuyama congenital muscular dystrophy	<i>FKTN</i>	mouse	VPMO	exon 10 aberrant 3'ss; alternative 5'ss; ESE (correct splicing)	IM	(<u>145</u>)
Hutchinson–Gilford progeria	<i>LMNA</i>	mouse	VPMO; 2'-MOE /PS	exon 10 5'ss; exon 11 cryptic 5'ss; exon 11 ESE (block exon 11 splicing)	IV/IP	(<u>146,147</u>)
Leber congenital amaurosis	<i>CEP290</i>	mouse	2'-OMe /PS; AAV	Intron 26 cryptic exon (correct splicing)	IVI	(<u>56</u>)
Myotonic dystrophy	<i>CLCN1</i>	mouse	PMO	exon 7a 3'ss (exon 7a skipping)	IM	(<u>53,148</u>)
Usher syndrome	<i>USH1C</i>	mouse	2'-MOE /PS	exon 3 cryptic 5'ss (correct	IP	(<u>40</u>)

Condition	Target gene	Stage/Model	SSO	Target (Action)	Route	Ref (see Haven's and Hastings)
				splicing)		
X-linked agammaglobulinemia	<i>BTK</i>	mouse	PPMO	pseudoexon 4A ESS (pseudoexon skipping)	IV/SC	(149)
Switch alternative splicing						
Alzheimer's disease	<i>LRP8</i>	mouse	2'-MOE /PS	intron 19 ISS (exon 19 inclusion)	ICV	(42)
Autoimmune diabetes susceptibility	<i>CTLA4</i>	mouse	PPMO	exon 2 3'ss (exon skipping)	IP	(150)
Cancer	<i>BCL2L1</i>	mouse	2'-MOE /PS	exon 2 5'ss (alternative 5'ss)	IV/NP	(151)
Cancer	<i>ERBB4</i>	mouse	LNA	exon 26 5'ss (exon skipping)	IP	(152)
Cancer	<i>MDM4</i>	mouse	PMO	exon 6 5'ss (exon skipping)	ITM	(153)
Cancer	<i>STAT3</i>	mouse	VPMO	exon 23 α 3'ss (β 3'ss use)	ITM	(154)

Condition	Target gene	Stage/Model	SSO	Target (Action)	Route	Ref (see Haven's and Hastings)
Inflammation	<i>IL1RAP</i>	mouse	2-OMe /PS;LNA	exon 9 ESE (exon skipping)	IV/NP	(155)
Inflammation	<i>TNFRSF1B</i>	mouse	LNA /PS	exon 7 5'ss (exon skipping)	IP	(156)
Neovascularization	<i>FLT1</i>	mouse	PMO	exon 13 5'ss (alternative pA site)	IVI / ITM	(157)
Neovascularization	<i>KDR</i>	mouse	PMO	exon 13 5'ss (alternative pA site)	IVI / SCJ	(158)
Spinal muscular atrophy	<i>SMN2</i>	clinical trials	2'-MOE /PS	intron 7 ISS (exon 7 inclusion)	IT	(43,142)
Correct open reading frame						
cardiomyopathy	<i>MYBPC3</i>	mouse	AAV	Exon 5 and 6 ESEs (exon 5, 6 skipping)	IV	(159)
Cardiomyopathy	<i>TTN</i>	mouse	VPMO	exon 326 ESE (exon skipping)	IP	(160)
Duchenne muscular dystrophy (DMD)	<i>DMD</i>	clinical trials	2'-OMe / PMO	exon 51 ESE (exon	IV/SC	(46,98)

Condition	Target gene	Stage/Mode I	SSO	Target (Action)	Route	Ref (see Haven's and Hastings)
				skipping)		
Nijmegen breakage syndrome	<i>NBN</i>	mouse	VPMO	exon 6/7 ESEs (exon skipping)	IV	(<u>161</u>)
Disrupt open reading frame/Protein function						
Ebola	<i>IL10</i>	mouse	PPMO	exon 4 3'ss (exon skipping)	IP	(<u>162</u>)
Huntington disease	<i>HTT</i>	mouse	2'-OMe /PS	exon 12 skipping	IS	(<u>163</u>)
Hypercholesterolemia	<i>APOB</i>	mouse	2'-OMe /PS	exon 27 3'ss (exon skipping)	IV	(<u>164</u>)
Muscle-Wasting/DMD	<i>MSTN</i>	mouse	PPMO/VPMO/ 2'-OMe	exon 2 ESE (exon skipping)	IV/ IM/ IP	(<u>165,166</u>)
Pompe disease	<i>GYS2</i>	mouse	PPMO	exon 6 5'ss (exon skipping)	IM/IV	(<u>167</u>)
Spinocerebellar ataxia type 3	<i>ATXN3</i>	mouse	2'-OMe /PS	exon 9, 10 skipping	ICV	(<u>168</u>)

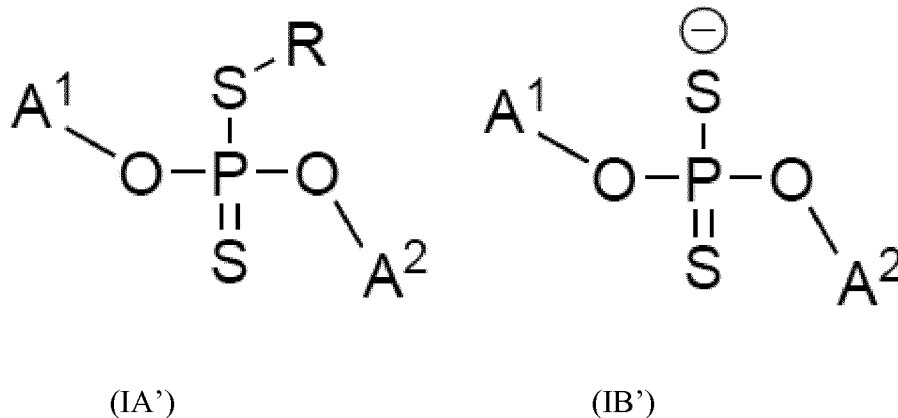
In some embodiments of the invention, the antisense oligonucleotide is a splice modulating oligonucleotide which is complementary to a pre-mRNA selected from the

group consisting of a HBB, FKTN, LMNA, CEP290, CLCN1, USH1C, BTK, LRP8, CTLA4, BCL2L1, ERBB4, MDM4, STAT3, IL1RAP, TNFRSF1B, FLT1, KDR, SMN2, MYBPC3, TTN, DMD, NBN, IL10, HTT, APOB, MSTN, GYS2, and ATXN3.

Exemplary diseases which may be treated with the SSOs of the invention, on a target by target basis are provided in Table A.

The following embodiments relate in general to single stranded antisense oligonucleotides of the invention, and splice modulating antisense oligonucleotide (SSOs) in particular:

1. A single stranded antisense oligonucleotide, for modulation of a RNA target in a cell, wherein the antisense oligonucleotide comprises or consists of a contiguous nucleotide sequence of 10 – 30 nucleotides in length, wherein the contiguous nucleotide sequence comprises one or more 2' sugar modified nucleosides, and wherein at least one of the internucleoside linkages present between the nucleosides of the contiguous nucleotide sequence is a phosphorodithioate linkage of formula IA or IB



wherein one of the two oxygen atoms is linked to the 3' carbon atom of an adjacent nucleoside (A^1) and the other one is linked to the 5' carbon atom of another adjacent nucleoside (A^2), and wherein R is hydrogen or a phosphate protecting group.

2. The antisense oligonucleotide according to embodiment 1, wherein at least one of the two nucleosides (A^1) and (A^2) is a 2' sugar modified nucleoside.
3. The antisense oligonucleotide according to embodiment 1, wherein both nucleosides (A^1) and (A^2) is a 2' sugar modified nucleoside.
4. The antisense oligonucleotide according to any one of embodiments 1 - 3, wherein at least one of the two nucleosides (A^1) and (A^2), or both nucleosides (A^1) and (A^2) is a DNA nucleoside.

5. The antisense oligonucleotide according to any one of embodiments 1 - 4, wherein at least one of (A¹) and (A²) is a 2'-sugar modified nucleoside or nucleosides are independently selected from 2'-alkoxy-RNA, 2'-alkoxyalkoxy-RNA, 2'-amino-DNA, 2'-fluoro-RNA, 2'-fluoro-ANA or a LNA nucleoside.
- 5 6. The antisense oligonucleotide according to any one of embodiments 1 - 5, wherein least one of (A¹) and (A²) is a LNA nucleoside.
7. The antisense oligonucleotide according to any one of embodiments 1 - 5, wherein both (A¹) and (A²) are LNA nucleosides.
8. The antisense oligonucleotide according to any one of embodiments 1 - 6, wherein
10 least one of (A¹) and (A²) is a 2'-O-methoxyethyl nucleoside.
9. The antisense oligonucleotide according to any one of embodiments 1 - 5, wherein both of (A¹) and (A²) is a 2'-O-methoxyethyl nucleoside.
10. The antisense oligonucleotide according to any one of embodiments 1 - 8, wherein the LNA nucleosides are selected from the group consisting of beta-D-oxy LNA, 6'-
15 methyl-beta- D-oxy LNA and ENA.
11. The antisense oligonucleotide according to any one of embodiments 1 - 8, wherein the LNA nucleosides are beta-D-oxy LNA.
12. The antisense oligonucleotide according to any one of embodiments 1 - 11, wherein the contiguous nucleotide sequence comprises one or more further 2'-sugar
20 modified nucleosides, such as one or more further 2'-sugar modified nucleosides selected from the group consisting of 2'-alkoxy-RNA, 2'-alkoxyalkoxy-RNA, 2'-amino-DNA, 2'-fluoro-RNA, 2'-fluoro-ANA or a LNA nucleoside.
13. The antisense oligonucleotide according to any one of embodiments 1-12, wherein the contiguous nucleotide sequence comprises both LNA nucleosides and DNA
25 nucleosides.
14. The antisense oligonucleotide according to any one of embodiments 1-12, wherein the contiguous nucleotide sequence comprises both LNA nucleosides and 2'-O-methoxyethyl nucleosides.
15. The antisense oligonucleotide according to any one of embodiments 1-13, wherein
30 the contiguous nucleotide sequence comprises both LNA nucleosides and 2'-fluoro RNA nucleosides.

16. The antisense oligonucleotide according to any one of embodiments 1-13, wherein the contiguous nucleotide sequence comprises either
- (i) only LNA and DNA nucleosides
 - (ii) only LNA and 2'-O-methoxyethyl nucleosides
 - 5 (iii) only LNA, DNA and 2'-O-methoxyethyl nucleosides
 - (iv) only LNA, 2'fluoro RNA and 2'-O-methoxyethyl nucleosides
 - (v) only LNA, DNA, 2'fluoro RNA and 2'-O-methoxyethyl nucleosides or only LNA, 2'fluoro RNA and 2'-O-methoxyethyl nucleosides
 - (vi) only 2'-O-methoxyethyl nucleosides.
- 10 17. The antisense oligonucleotide according to any one of embodiments 1- 16, wherein the contiguous nucleotide sequence does not comprise a sequence of 4 or more contiguous DNA nucleosides, or does not comprise a sequence of three or more contiguous DNA nucleosides.
- 15 18. The antisense oligonucleotide according to any one of embodiments 1 – 17, wherein the antisense oligonucleotide or the contiguous nucleotide sequence thereof is a mixmer oligonucleotide or a totalmer oligonucleotide.
19. The antisense oligonucleotide according to any one of embodiments 1- 18, wherein the antisense oligonucleotide is not capable of recruiting human RNaseH1.
- 20 20. The antisense oligonucleotide according to any one of embodiments 1 – 19, wherein the nucleoside (A^2) is the 3' terminal nucleoside of the contiguous nucleotide sequence or of the oligonucleotide.
21. The antisense oligonucleotide according to any one of embodiments 1 – 20, wherein the nucleoside (A^1) is the 5' terminal nucleoside of the contiguous nucleotide sequence or of the oligonucleotide.
- 25 22. The antisense oligonucleotide according to any one of embodiments 1 – 21, which comprises at least two phosphorodithioate internucleoside linkage of formula I, such as 2, 3, 4, 5, or 6 phosphorodithioate internucleoside linkage of formula I.
23. The antisense oligonucleotide according to any one of embodiments 1 – 22, wherein the internucleoside linkage between the 2 3' most nucleosides of the contiguous
30 nucleotide sequence is a phosphorodithioate internucleoside linkage of formula I, and wherein the internucleoside linkage between the 2 5' most nucleosides of the

contiguous nucleotide sequence is a phosphorodithioate internucleoside linkage of formula I.

24. The antisense oligonucleotide according to any one of embodiments 1 -23 which further comprises phosphorothioate internucleoside linkages.
- 5 25. The antisense oligonucleotide according to any one of embodiments 1 -24 which further comprises stereodefined phosphorothioate internucleoside linkages.
26. The antisense oligonucleotide according to any one of embodiments 1 -25, wherein the remaining internucleoside linkages are independently selected from the group consisting of phosphorodithioate internucleoside linkages, phosphorothioate internucleoside linkages, and phosphodiester internucleoside linkages.
- 10 27. The antisense oligonucleotide according to any one of embodiments 1 -26, wherein the remaining internucleoside linkages are phosphorothioate internucleoside linkages.
28. The antisense oligonucleotide according to any one of embodiments 1 -27, wherein said contiguous nucleotide sequence is complementary, such as 100% complementary, to a mammalian pre-mRNA, a mammalian mature mRNA target, a viral RNA target, or a mammalian long non coding RNA.
- 15 29. The antisense oligonucleotide according to any one of embodiments 28, wherein the RNA target is a human RNA target.
- 20 30. The antisense oligonucleotide according to any one of embodiments 1 – 29, wherein the antisense oligonucleotide modulates the splicing of a mammalian, such as human pre-mRNA target, e.g. is a splice skipping or splice modulating antisense oligonucleotide.
31. The antisense oligonucleotide according to any one of embodiments 1 – 30, wherein the antisense oligonucleotide is complementary, such as 100% complementary to a intron/exon splice site of a human pre-mRNA, or a splice modulating region of a human pre-mRNA.
- 25 32. The antisense oligonucleotide according to any one of embodiments 1 – 30, wherein the antisense oligonucleotide or contiguous nucleotide sequence thereof is complementary, such as fully complementary to a human pre-mRNA sequence selected from the group consisting of TNFR2, HBB, FKTN, LMNA, CEP290, CLCN1, USH1C, BTK, LRP8, CTLA4, BCL2L1, ERBB4, MDM4, STAT3,
- 30

IL1RAP, TNFRSF1B, FLT1, KDR, SMN2, MYBPC3, TTN, DMD, NBN, IL10, HTT, APOB, MSTN, GYS2, and ATXN3.

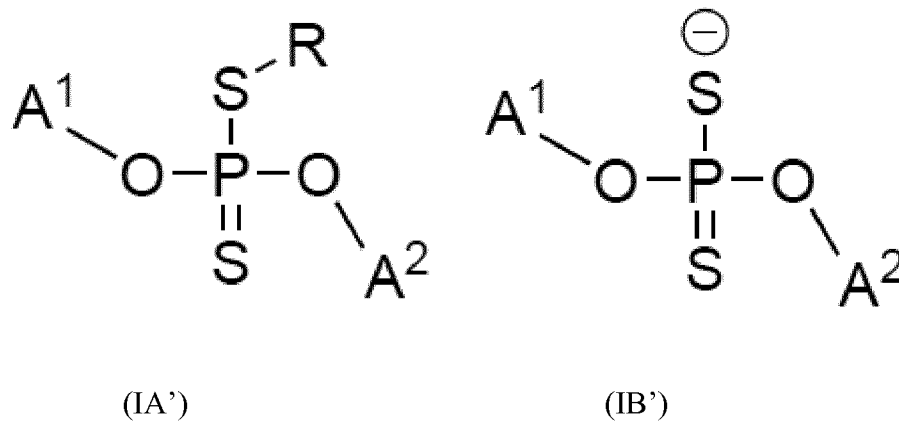
33. The antisense oligonucleotide according to any one of embodiments 1 – 32, wherein the antisense oligonucleotide consists or comprises of a contiguous nucleotide sequence selected from the group consisting of SSO#1 – SSO#25
34. The antisense oligonucleotide according to any one of embodiments 1 – 33, wherein the cell is a human cell.
35. The antisense oligonucleotide according to any one of embodiments 1 – 34, wherein the length of the antisense oligonucleotide is 10 – 30 nucleotides in length.
36. The antisense oligonucleotide according to any one of embodiments 1 – 34, wherein the length of the antisense oligonucleotide is 12 – 24 nucleotides in length.
37. The antisense oligonucleotide according to any one of embodiments 1 – 36, wherein the 3' terminal nucleoside of the antisense oligonucleotide or the antisense oligonucleotide or the contiguous nucleotide sequence thereof is either a LNA nucleoside or a 2-O-methoxyethyl nucleoside.
38. The antisense oligonucleotide according to any one of embodiments 1 – 27, wherein the 5' terminal nucleoside of the antisense oligonucleotide or the contiguous nucleotide sequence thereof is either a LNA nucleoside or a 2-O-methoxyethyl nucleoside.
39. The antisense oligonucleotide according any one of embodiments 1 – 38, wherein the 5' terminal nucleoside and the 3' terminal nucleoside of the antisense oligonucleotide or the contiguous nucleotide sequence thereof are both LNA nucleosides.
40. The antisense oligonucleotide according any one of embodiments 1 – 39, wherein the contiguous nucleotide sequence comprises at least one region of two or three LNA contiguous nucleotides, and/or at least one region of two or three contiguous 2'-O-methoxyethyl contiguous nucleotides.
41. A pharmaceutically acceptable salt of an oligonucleotide according to any one of embodiments 1 to 40, in particular a sodium or a potassium salt or an ammonium salt.
42. A conjugate comprising an oligonucleotide or a pharmaceutically acceptable salt according to any one of embodiments 1 to 41 and at least one conjugate moiety

covalently attached to said oligonucleotide or said pharmaceutically acceptable salt, optionally *via* a linker moiety.

43. A pharmaceutical composition comprising an oligonucleotide, pharmaceutically acceptable salt or conjugate according to any one of embodiments 1 to 42 and a therapeutically inert carrier.
44. An oligonucleotide, pharmaceutically acceptable salt or conjugate according to any one of embodiments 1 to 43 for use as a therapeutically active substance.
45. A method for the modulation of a target RNA in a cell which is expressing said RNA, said method comprising the step of administering an effective amount of the oligonucleotide, pharmaceutically acceptable salt, conjugate or composition according to any one of embodiments 1 – 44 to the cell.
46. A method for the modulation of a splicing of a target pre-RNA in a cell which is expressing said target pre-mRNA, said method comprising the step of administering an effective amount of the oligonucleotide, pharmaceutically acceptable salt, conjugate or composition according to any one of embodiments 1 – 44 to the cell.
47. The method according to embodiments 45 or 46 wherein said method is an in vitro method or an in vivo method.
48. Use of an oligonucleotide, pharmaceutical salt, conjugate, or composition of any one of embodiments 1 – 44, for inhibition of a RNA in a cell, such as in a human cell, wherein said use is in vitro or in vivo.

CERTAIN MIXMER EMBODIMENTS

1. A single stranded antisense oligonucleotide, for modulation of a RNA target in a cell, wherein the antisense oligonucleotide comprises or consists of a contiguous nucleotide sequence of 10 – 30 nucleotides in length, wherein the contiguous nucleotide sequence comprises alternating regions of 2'sugar modified nucleosides, wherein the maximum length of contiguous DNA nucleoside with the contiguous nucleotide sequence is 3 or 4, and wherein at least one of the internucleoside linkages present between the nucleosides of the contiguous nucleotide sequence is a phosphorodithioate linkage of formula IA or IB



wherein one of the two oxygen atoms is linked to the 3' carbon atom of an adjacent nucleoside (A¹) and the other one is linked to the 5' carbon atom of another adjacent nucleoside (A²), and wherein R is hydrogen or a phosphate protecting group.

2. The antisense oligonucleotide according to embodiment 1, wherein at least one of the two nucleosides (A¹) and (A²) is a 2' sugar modified nucleoside.
3. The antisense oligonucleotide according to embodiment 1, wherein both nucleosides (A¹) and (A²) is a 2' sugar modified nucleoside.
- 10 4. The antisense oligonucleotide according to any one of embodiments 1 - 3, wherein at least one of the two nucleosides (A¹) and (A²), or both nucleosides (A¹) and (A²) is a DNA nucleoside.
5. The antisense oligonucleotide according to any one of embodiments 1 - 4, wherein at least one of (A¹) and (A²) is a 2'-sugar modified nucleoside or nucleosides are independently selected from 2'-alkoxy-RNA, 2'-alkoxyalkoxy-RNA, 2'-amino-DNA, 2'-fluoro-RNA, 2'-fluoro-ANA or a LNA nucleoside.
- 15 6. The antisense oligonucleotide according to any one of embodiments 1 - 5, wherein least one of (A¹) and (A²) is a LNA nucleoside.
7. The antisense oligonucleotide according to any one of embodiments 1 - 5, wherein both (A¹) and (A²) are LNA nucleosides.
- 20 8. The antisense oligonucleotide according to any one of embodiments 1 - 6, wherein least one of (A¹) and (A²) is a 2'-O-methoxyethyl nucleoside.
9. The antisense oligonucleotide according to any one of embodiments 1 - 5, wherein both of (A¹) and (A²) is a 2'-O-methoxyethyl nucleoside.

10. The antisense oligonucleotide according to any one of embodiments 1 – 8, wherein the LNA nucleosides are selected from the group consisting of beta-D-oxy LNA, 6'-methyl-beta- D-oxy LNA and ENA.
- 5 11. The antisense oligonucleotide according to any one of embodiments 1 – 8, wherein the LNA nucleosides are beta-D-oxy LNA.
12. The antisense oligonucleotide according to any one of embodiments 1 – 11, wherein the contiguous nucleotide sequence comprises one or more further 2'-sugar modified nucleosides, such as one or more further 2'sugar modified nucleosides selected from the group consisting of 2'-alkoxy-RNA, 2'-alkoxyalkoxy-RNA, 2'-amino-DNA, 2'-fluoro-RNA, 2'-fluoro-ANA or a LNA nucleoside.
- 10 13. The antisense oligonucleotide according to any one of embodiments 1-12, wherein the contiguous nucleotide sequence comprises both LNA nucleosides and DNA nucleosides.
14. The antisense oligonucleotide according to any one of embodiments 1- 12, wherein the contiguous nucleotide sequence comprises both LNA nucleosides and 2'-O-methoxyethyl nucleosides.
- 15 15. The antisense oligonucleotide according to any one of embodiments 1- 13, wherein the contiguous nucleotide sequence comprises both LNA nucleosides and 2'fluoro RNA nucleosides.
- 20 16. The antisense oligonucleotide according to any one of embodiments 1- 13, wherein the contiguous nucleotide sequence comprises either
 - (i) LNA and DNA nucleosides
 - (ii) LNA, DNA and 2'-O-methoxyethyl nucleosides or
 - (iii) LNA, DNA, 2'fluoro RNA and 2'-O-methoxyethyl nucleosides .
- 25 17. The antisense oligonucleotide according to any one of embodiments 1- 16, wherein the contiguous nucleotide sequence does not comprise a sequence of 3 or more contiguous DNA nucleosides, or does not comprise a sequence of 2 or more contiguous DNA nucleosides.
- 30 18. The antisense oligonucleotide according to any one of embodiments 1 – 17, wherein the antisense oligonucleotide or the contiguous nucleotide sequence thereof is a mixmer oligonucleotide, such as a splice modulating oligonucleotide or a microRNA inhibitor oligonucleotide.

25. The antisense oligonucleotide according to any one of embodiments 1 – 24, which comprises at least two phosphorodithioate internucleoside linkage of formula I, such as 2, 3, 4, 5, or 6 phosphorodithioate internucleoside linkage of formula I.
- 5 26. The antisense oligonucleotide according to any one of embodiments 1 – 25, wherein the contiguous nucleotide sequence comprises two contiguous DNA nucleotides wherein the nucleoside linkage between the two contiguous DNA nucleotides is a phosphorodithioate internucleoside linkage of formula IA or IB, i.e. a P2S linked DNA nucleotide pair.
- 10 27. The antisense oligonucleotide according to any one of embodiments 1 – 26, wherein the contiguous nucleotide sequence comprises more than one P2S linked DNA nucleotide pair.
- 15 28. The antisense oligonucleotide according to any one of embodiments 1 – 26, wherein all the nucleosides linkage between the two contiguous DNA nucleotides present in the contiguous nucleotide sequence are phosphorodithioate internucleoside linkage of formula IA or IB.
29. The antisense oligonucleotide according to any one of embodiments 1 – 27, wherein at least one internucleoside linkage between a 2'sugar modified nucleoside and a DNA nucleoside are phosphorodithioate internucleoside linkage of formula IA or IB.
- 20 30. The antisense oligonucleotide according to any one of embodiments 1 – 27, wherein more than one internucleoside linkage between a 2'sugar modified nucleoside and a DNA nucleoside are phosphorodithioate internucleoside linkage of formula IA or IB.
- 25 31. The antisense oligonucleotide according to any one of embodiments 1 – 27, wherein all internucleoside linkages between a 2'sugar modified nucleoside and a DNA nucleoside are phosphorodithioate internucleoside linkage of formula IA or IB.
- 30 32. The antisense oligonucleotide according to any one of embodiments 1 – 27, wherein at least one of the internucleoside linkages between a two 2'sugar modified nucleosides is not a phosphorodithioate internucleoside linkage of formula IA or IB, such as is a phosphorothioate internucleoside linkage.
33. The antisense oligonucleotide according to any one of embodiments 1 – 27, wherein all of the internucleoside linkages between two 2'sugar modified nucleosides are not a phosphorodithioate internucleoside linkage of formula IA or IB, such as are phosphorothioate internucleoside linkages.

34. The antisense oligonucleotide according to any one of embodiments 1 – 33, wherein the internucleoside linkage between the 2' 3' most nucleosides of the contiguous nucleotide sequence is a phosphorodithioate internucleoside linkage of formula I, and wherein the internucleoside linkage between the 2' 5' most nucleosides of the contiguous nucleotide sequence is a phosphorodithioate internucleoside linkage of formula I.
35. The antisense oligonucleotide according to any one of embodiments 1 -34 which further comprises phosphorothioate internucleoside linkages.
36. The antisense oligonucleotide according to any one of embodiments 1 -35 which further comprises stereodefined phosphorothioate internucleoside linkages.
37. The antisense oligonucleotide according to any one of embodiments 1 -35, wherein the remaining internucleoside linkages are independently selected from the group consisting of phosphorodithioate internucleoside linkages, phosphorothioate internucleoside linkages, and phosphodiester internucleoside linkages.
38. The antisense oligonucleotide according to any one of embodiments 1 -36, wherein the remaining internucleoside linkages are phosphorothioate internucleoside linkages.
39. The antisense oligonucleotide according to any one of embodiments 1 -37, wherein said contiguous nucleotide sequence is complementary, such as 100% complementary, to a mammalian such as a human pre-mRNA.
40. The antisense oligonucleotide according to any one of embodiments 1 – 38, wherein the antisense oligonucleotide modulates the splicing of a mammalian, such as human pre-mRNA target, e.g. is a splice skipping or splice modulating antisense oligonucleotide.
41. The antisense oligonucleotide according to any one of embodiments 1 – 39, wherein the antisense oligonucleotide is complementary, such as 100% complementary to a intron/exon splice site of a human pre-mRNA, or a splice modulating region of a human pre-mRNA.
42. The antisense oligonucleotide according to any one of embodiments 1 –41, wherein the antisense oligonucleotide or contiguous nucleotide sequence thereof is complementary, such as fully complementary to a human pre-mRNA sequence selected from the group consisting of TNFR2, HBB, FKTN, LMNA, CEP290, CLCN1, USH1C, BTK, LRP8, CTLA4, BCL2L1, ERBB4, MDM4, STAT3,

IL1RAP, TNFRSF1B, FLT1, KDR, SMN2, MYBPC3, TTN, DMD, NBN, IL10, HTT, APOB, MSTN, GYS2, and ATXN3.

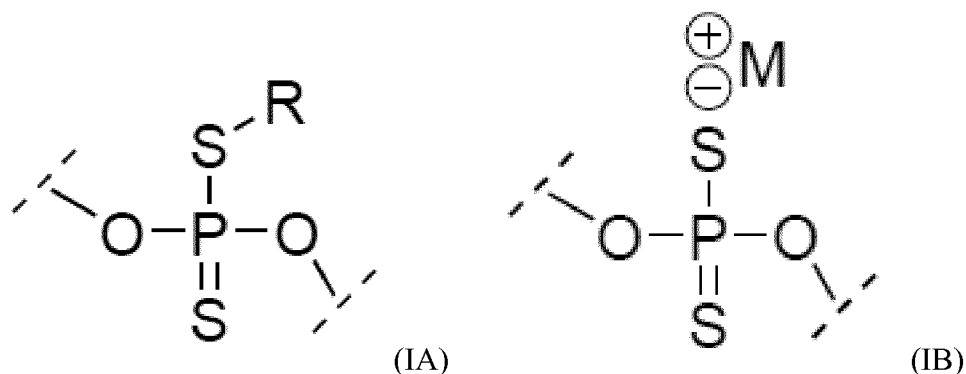
43. The antisense oligonucleotide according to any one of embodiments 1 – 42, wherein the antisense oligonucleotide consists or comprises of a contiguous nucleotide sequence selected from the group consisting of SSO#1 – SSO#25
44. The antisense oligonucleotide according to any one of embodiments 1 – 43, wherein the cell is a mammalian cell.
45. The antisense oligonucleotide according to any one of embodiments 1 – 44, wherein the length of the antisense oligonucleotide is 10 – 30 nucleotides in length.
46. The antisense oligonucleotide according to any one of embodiments 1 – 44, wherein the length of the antisense oligonucleotide is 12 – 24 nucleotides in length.
47. The antisense oligonucleotide according to any one of embodiments 1 – 46, wherein the 3' terminal nucleoside of the antisense oligonucleotide or the antisense oligonucleotide or the contiguous nucleotide sequence thereof is either a LNA nucleoside or a 2-O-methoxyethyl nucleoside.
48. The antisense oligonucleotide according to any one of embodiments 1 – 47, wherein the 5' terminal nucleoside of the antisense oligonucleotide or the contiguous nucleotide sequence thereof is either a LNA nucleoside or a 2-O-methoxyethyl nucleoside.
49. The antisense oligonucleotide according any one of embodiments 1 – 48, wherein the 5' terminal nucleoside and the 3' terminal nucleoside of the antisense oligonucleotide or the contiguous nucleotide sequence thereof are both LNA nucleosides.
50. The antisense oligonucleotide according any one of embodiments 1 – 49, wherein the contiguous nucleotide sequence comprises at least one region of two or three LNA contiguous nucleotides, and/or at least one region of two or three contiguous 2'-O-methoxyethyl contiguous nucleotides.
51. A pharmaceutically acceptable salt of an oligonucleotide according to any one of embodiments 1 to 50, in particular a sodium or a potassium salt or an ammonium salt.
52. A conjugate comprising an oligonucleotide or a pharmaceutically acceptable salt according to any one of embodiments 1 to 51 and at least one conjugate moiety

covalently attached to said oligonucleotide or said pharmaceutically acceptable salt, optionally via a linker moiety.

53. A pharmaceutical composition comprising an oligonucleotide, pharmaceutically acceptable salt or conjugate according to any one of embodiments 1 to 52 and a therapeutically inert carrier.
54. An oligonucleotide, pharmaceutically acceptable salt or conjugate according to any one of embodiments 1 to 53 for use as a therapeutically active substance.
55. A method for the modulation of a target RNA in a cell which is expressing said RNA, said method comprising the step of administering an effective amount of the oligonucleotide, pharmaceutically acceptable salt, conjugate or composition according to any one of embodiments 1 – 54 to the cell.
56. A method for the modulation of a splicing of a target pre-RNA in a cell which is expressing said target pre-mRNA, said method comprising the step of administering an effective amount of the oligonucleotide, pharmaceutically acceptable salt, conjugate or composition according to any one of embodiments 1 – 54 to the cell.
57. The method according to embodiments 55 or 56 wherein said method is an in vitro method or an in vivo method.
58. Use of an oligonucleotide, pharmaceutical salt, conjugate, or composition of any one of embodiments 1 – 54, for inhibition of a RNA in a cell, such as in a mammalian cell, wherein said use is in vitro or in vivo.

CERTAIN EMBODIMENTS RELATING TO 3' END PROTECTION

1. A single stranded antisense oligonucleotide comprising at least one phosphorodithioate internucleoside linkage of formula IA or IB



- wherein one of the two oxygen atoms is linked to the 3' carbon atom of an adjacent nucleoside (A^1) and the other one is linked to the 5' carbon atom of another adjacent

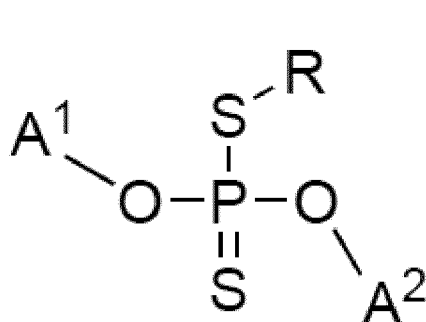
- nucleoside (A^2), and wherein in (IA) R is hydrogen or a phosphate protecting group, and in (IB) M^+ is a cation, such as a metal cation, such as an alkali metal cation, such as a Na^+ or K^+ cation; or M^+ is an ammonium cation, and wherein at least one of the two nucleosides (A^1) and (A^2) is a 2' sugar modified nucleoside, such as a LNA nucleoside or a 2'-O-MOE nucleoside, and wherein R is hydrogen or a phosphate protecting group, wherein A^2 is the 3' terminal nucleoside of the oligonucleotide.
- 5
2. The single stranded antisense according to embodiment 1, wherein (A^2) is a LNA nucleoside, or both (A^1) and (A^2) are LNA nucleosides.
 - 10 3. The single stranded antisense according to embodiment 1, wherein (A^2) is a LNA nucleoside and (A^1) is a sugar modified nucleotide.
 4. The single stranded antisense according to embodiment 1, wherein (A^2) is a LNA nucleoside and (A^1) is DNA nucleotide.
 5. The single stranded antisense according to embodiment 1, wherein (A^1) is a LNA nucleoside and (A^2) is a sugar modified nucleotide.
 - 15 6. The single stranded antisense according to embodiment 1, wherein (A^1) is a LNA nucleoside and (A^2) is a DNA nucleotide.
 7. The single stranded antisense according to any one of embodiments 3 or 5, wherein said sugar modified nucleoside is a 2'-sugar modified nucleoside.
 - 20 8. The single stranded antisense according to embodiment 7, wherein said 2'-sugar modified nucleoside is 2'-alkoxy-RNA, 2'-alkoxyalkoxy-RNA, 2'-amino-DNA, 2'-fluoro-RNA, 2'-fluoro-ANA or a LNA nucleoside.
 9. The single stranded antisense according to embodiment 7 or 8, wherein said 2'-sugar modified nucleoside is a 2'-O-methoxyethyl nucleoside.
 - 25 10. The single stranded antisense according to any one of embodiments 1 - 9, wherein the LNA nucleoside or nucleotides are in the beta-D configuration.
 11. The single stranded antisense according to any one of embodiments 1 to 10, wherein the LNA nucleosides are independently selected from beta-D-oxy LNA, 6'-methyl-beta-D-oxy LNA and ENA.
 - 30 12. The single stranded antisense according to any one of embodiment 1 to 11, wherein LNA is beta-D-oxy LNA.

13. The single stranded antisense according to any one of embodiments 1 – 12, wherein the single stranded antisense consists or comprises of 7 – 30 contiguous nucleotides which are complementary to a target nucleic acid, such as a target nucleic acid selected from the group consisting of a pre-mRNA, and mRNA, a microRNA, a viral RNA, and a long non coding RNA [referred to as the contiguous nucleotide sequence of an antisense single stranded antisense].
14. The single stranded antisense according to any one of embodiments 1 to 13, wherein the contiguous nucleotide sequence comprises a gapmer region of formula 5'-F-G-F'-3', wherein G is a region of 5 to 18 nucleosides which is capable of recruiting RnaseH, and said region G is flanked 5' and 3' by flanking regions F and F' respectively, wherein regions F and F' independently comprise or consist of 1 to 7 2'-sugar modified nucleotides, wherein the nucleoside of region F which is adjacent to region G is a 2'-sugar modified nucleoside and wherein the nucleoside of region F' which is adjacent to region G is a 2'-sugar modified nucleoside. .
15. 14. The single stranded antisense according to any one of embodiments 1 to 13, wherein the contiguous nucleotide sequence is a mixmer oligonucleotide, wherein the mixmer oligonucleotide comprises both LNA nucleosides and DNA nucleoside, and optionally 2'sugar modified nucleosides [such as those according to embodiments 8 – 9], wherein the single stranded antisense does not comprise a region of 4 or more contiguous DNA nucleosides.
16. The oligonucleotide according to embodiment 14 or 15, wherein the oligonucleotide is a splice modulating oligonucleotide [capable of modulating the splicing of a pre-mRNA splice event].
17. The oligonucleotide according to embodiment 14 or 15, wherein the oligonucleotide is complementary to a microRNA, such as is a microRNA inhibitor.
18. An oligonucleotide according to any one of embodiments 1 to 17, comprising further internucleoside linkages independently selected from phosphodiester internucleoside linkage, phosphorothioate internucleoside linkage and phosphorodithioate internucleoside linkages; or wherein the further internucleoside linkages within the oligonucleotide or within the contiguous nucleotide sequence thereof, are independently selected from phosphorothioate internucleoside linkage and phosphorodithioate internucleoside linkages.

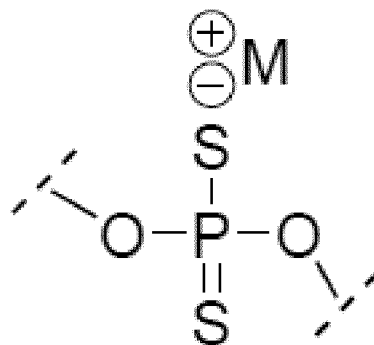
18. An oligonucleotide according to any one of embodiments 1 - 18, wherein the further internucleoside linkages of the oligonucleotide, or contiguous nucleotide sequence thereof, are all phosphorothioate internucleoside linkages.
19. The oligonucleotide according to any one of embodiments 1 – 18, wherein the oligonucleotide comprises a 5' region position 5' to the contiguous nucleotide sequence, wherein the 5' nucleoside region comprises at least one phosphodiester linkage.
20. The oligonucleotide according to embodiment 19, wherein the 5' region comprises 1 – 5 phosphodiester linked DNA nucleosides, and optionally may link the oligonucleotide or contiguous nucleotide sequence thereof to a conjugate moiety.
21. The oligonucleotide according to any one of embodiments 1 to 20, wherein one or more nucleoside is a nucleobase modified nucleoside.
22. The oligonucleotide according to any one of embodiments 1 to 21, wherein one or more nucleoside is 5-methyl cytosine, such as a LNA 5-methyl cytosine or a DNA 5-methyl cytosine.
23. A pharmaceutically acceptable salt of an oligonucleotide according to any one of embodiments 1 to 22, in particular a sodium or a potassium salt or ammonium salt.
24. A conjugate comprising an oligonucleotide or a pharmaceutically acceptable salt according to any one of embodiments 1 to 23 and at least one conjugate moiety covalently attached to said oligonucleotide or said pharmaceutically acceptable salt, optionally *via* a linker moiety.
25. A pharmaceutical composition comprising an oligonucleotide, pharmaceutically acceptable salt or conjugate according to any one of embodiments 1 to 24 and a therapeutically inert carrier.
26. An oligonucleotide, pharmaceutically acceptable salt or conjugate according to any one of embodiments 1 to 25 for use as a therapeutically active substance.
27. The oligonucleotide, pharmaceutically acceptable salt or conjugate according to any one of embodiments 1 to 24 for use in therapy, for administration to a subject via parenteral administration, such as, intravenous, subcutaneous, intra-muscular, intracerebral, intracerebroventricular or intrathecal administration.

EMBODIMENTS RELATING TO OLIGONUCLEOTIDES WITH ACHIRAL PHOSPHORODITHIOATE AND STEREODEFINED PHOSPHOROTHIOATE LINKAGES

1. A single stranded antisense oligonucleotide comprising at least one phosphorodithioate internucleoside linkage of formula IA or IB

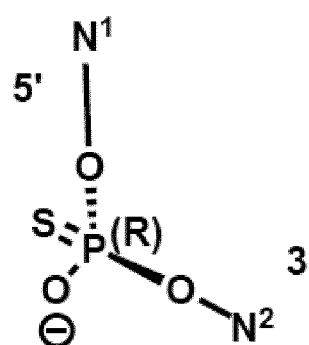
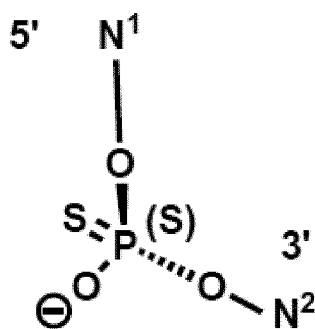


(IA')



(IB')

- 5 wherein one of the two oxygen atoms is linked to the 3' carbon atom of an adjacent nucleoside (A1) and the other one is linked to the 5' carbon atom of another adjacent nucleoside (A2), and wherein in (IA) R is hydrogen or a phosphate protecting group, and in (IB) M⁺ is a cation, such as a metal cation, such as an alkali metal cation, such as a Na⁺ or K⁺ cation; or M⁺ is an ammonium cation, and wherein the single
- 10 stranded oligonucleotide further comprises at least one stereodefined phosphorothioate internucleoside linkage, (Sp, S) or (Rp, R)



wherein N¹ and N² are nucleosides. (Note: In some non limiting embodiments N¹ and/or N² are DNA nucleotides).

- 15 2. The single stranded antisense oligonucleotide according to embodiment 1, wherein A2 is the 3' terminal nucleoside of the oligonucleotide.
3. The single stranded antisense oligonucleotide according to embodiment 1, wherein A1 is the 5' terminal nucleoside of the oligonucleotide.

4. The single stranded antisense oligonucleotide according to anyone of embodiments 1 – 3, wherein said single stranded oligonucleotide comprises 1, 2, 3, 4, 5, or 6 internucleoside linkages of formula IB.
5. The single stranded antisense oligonucleotide according to anyone of embodiments 1 – 4, wherein both the 5' most internucleoside linkage of the antisense oligonucleotide, and the 3' most internucleoside linkage of the antisense oligonucleotide are internucleoside linkages of formula IB.
6. The single stranded antisense oligonucleotide according to any one of embodiments 1 - 5, wherein in at least one of the internucleoside linkages of formula IB, at least one of the two nucleosides (A1) and (A2) is a 2' sugar modified nucleoside, such as a 2' sugar modified nucleoside selected from the group consisting of 2'-alkoxy-RNA, 2'-alkoxyalkoxy-RNA, 2'-amino-DNA, 2'-fluoro-RNA, 2'-fluoro-ANA and a LNA nucleoside.
7. The single stranded antisense oligonucleotide according to any one of embodiments 1 - 6, wherein in at least one of the internucleoside linkages of formula IB, at least one of the two nucleosides (A1) and (A2) is a LNA nucleoside.
8. The single stranded antisense oligonucleotide according to any one of embodiments 1 - 6, wherein in at least one of the internucleoside linkages of formula IB, at least one of the two nucleosides (A1) and (A2) is a 2'-O-MOE nucleoside.
9. The single stranded antisense oligonucleotide according to any one of embodiments 1 - 8, wherein the 3' terminal nucleoside of the antisense oligonucleotide is a LNA nucleoside or a 2'-O-MOE nucleoside.
10. The single stranded antisense oligonucleotide according to any one of embodiments 1 - 9, wherein the 5' terminal nucleoside of the antisense oligonucleotide is a LNA nucleoside or a 2'-O-MOE nucleoside.
11. The single stranded antisense oligonucleotide according to any one or embodiments 1 – 10, wherein the two 3' most terminal nucleosides of the antisense oligonucleotide are independently selected from LNA nucleosides and 2'-O-MOE nucleosides.
12. The single stranded antisense oligonucleotide according to any one or embodiments 1 – 11, wherein the two 5' most terminal nucleosides of the antisense oligonucleotide are independently selected from LNA nucleosides and 2'-O-MOE nucleosides.
13. The single stranded antisense oligonucleotide according to any one or embodiments 1 – 12, wherein the three 3' most terminal nucleosides of the antisense

oligonucleotide are independently selected from LNA nucleosides and 2'-O-MOE nucleosides.

14. The single stranded antisense oligonucleotide according to any one or embodiments 1 – 13, wherein the three 5' most terminal nucleosides of the antisense
5 oligonucleotide are independently selected from LNA nucleosides and 2'-O-MOE nucleosides.
15. The single stranded antisense oligonucleotide according to any one or embodiments 1 – 14, wherein the two 3' most terminal nucleosides of the antisense oligonucleotide are LNA nucleosides.
- 10 16. The single stranded oligonucleotide according to any one or embodiments 1 – 15, wherein the two 5' most terminal nucleosides of the antisense oligonucleotide are LNA nucleosides.
17. The single stranded antisense oligonucleotide according to any one of embodiments 1 – 16, wherein the antisense oligonucleotide further comprises a region of 2 – 16
15 DNA nucleotides, wherein the internucleoside linkages between the DNA nucleotides are stereodefined phosphorothioate internucleoside linkages.
18. The single stranded antisense oligonucleotide according to any one of embodiments 1 to 17, wherein the LNA nucleosides are independently selected from beta-D-oxy LNA, 6'-methyl-beta- D-oxy LNA and ENA.
- 20 19. The single stranded antisense oligonucleotide according to any one of embodiments 1 to 17, wherein the LNA nucleosides are beta-D-oxy LNA
20. The single stranded antisense oligonucleotide according to any one of embodiments 1 – 19, wherein the oligonucleotide consists or comprises of 7 – 30 contiguous
25 nucleotides which are complementary to, such as fully complementary to a target nucleic acid, such as a target nucleic acid selected from the group consisting of a pre-mRNA, and mRNA, a microRNA, a viral RNA, and a long non coding RNA [the antisense oligonucleotide].
21. The single stranded antisense oligonucleotide according to any one of embodiments 1 – 20, wherein the single stranded oligonucleotide is capable of modulating the
30 RNA target.
22. The single stranded antisense oligonucleotide according to any one of embodiments 1 – 20, wherein the single stranded antisense oligonucleotide is capable of inhibiting the RNA target, such as via RNase H1 recruitment.

23. The single stranded antisense oligonucleotide according to any one of embodiments 1 to 22, wherein the contiguous nucleotide sequence of the oligonucleotide comprises a gapmer region of formula 5'-F-G-F'-3', wherein G is a region of 5 to 18 nucleosides which is capable of recruiting RNaseH1, and said region G is flanked 5' and 3' by flanking regions F and F' respectively, wherein regions F and F' independently comprise or consist of 1 to 7 2'-sugar modified nucleotides, wherein the nucleoside of region F which is adjacent to region G is a 2'-sugar modified nucleoside and wherein the nucleoside of region F' which is adjacent to region G is a 2'-sugar modified nucleoside.
24. The single stranded antisense oligonucleotide according to embodiment 23, regions F or region F' comprise an internucleoside linkage of formula IB, according to any one of embodiments 1- 19.
25. The single stranded antisense oligonucleotide according to embodiment 24, wherein both of regions F and F' comprise an internucleoside linkage of formula IB, according to any one of embodiments 1- 19.
26. The single stranded antisense oligonucleotide according to embodiment 23 - 25, wherein all the internucleoside linkages within regions F and/or F' are internucleoside linkage of formula IB, according to any one of embodiments 1- 19.
27. The single stranded antisense oligonucleotide according to embodiments 23 - 26, wherein regions F and F' both comprise or consist of LNA nucleosides.
28. The single stranded antisense oligonucleotide according to embodiments 23 - 27, wherein regions F and F' both comprise or consist of MOE nucleosides.
29. The single stranded antisense oligonucleotide according to embodiments 23 - 28, wherein regions F comprises LNA nucleoside(s) and F' comprise or consist of MOE nucleosides.
30. The single stranded antisense oligonucleotide according to embodiments 23 - 29, wherein region G further comprises at least one internucleoside linkage of formula IB positioned between the 3' most nucleoside of region F and the 5' most nucleoside of region G.
31. The single stranded antisense oligonucleotide according to embodiments 23 - 30, wherein region G comprises at least one stereodefined phosphorothioate linkage positioned between two DNA nucleosides.

32. The single stranded antisense oligonucleotide according to embodiments 23 – 31, wherein region G comprises at least one internucleoside linkage of formula IB positioned between two DNA nucleosides.
- 5 33. The single stranded antisense oligonucleotide according to embodiments 23 – 32, wherein region G further comprises at least 2, 3, or 4 internucleoside linkages of formula IB.
- 10 34. The single stranded antisense oligonucleotide according to embodiments 23 – 31, wherein all the remaining internucleoside linkages within region G are stereodefined phosphorothioate internucleoside linkages, independently selected from Rp and Sp internucleoside linkages.
- 15 35. The single stranded antisense oligonucleotide according to embodiments 23 – 31, wherein all the internucleoside linkages within region G are stereodefined phosphorothioate internucleoside linkages, independently selected from Rp and Sp internucleoside linkages, optionally other than the internucleoside linkage between the 3' most nucleoside of region F and the 5' most nucleoside of region G.
36. The single stranded antisense oligonucleotide according to any one of embodiments 1 to 22, wherein the antisense oligonucleotide comprises less than 4 contiguous DNA nucleotides.
- 20 37. The single stranded antisense oligonucleotide according to any one of embodiments 1 to 22 or 36, wherein the antisense oligonucleotide is a mixmer or a totalmer oligonucleotide.
- 25 38. The single stranded oligonucleotide according to embodiment 37 wherein the mixmer oligonucleotide comprises both LNA nucleosides and DNA nucleosides, and optionally 2'sugar modified nucleosides (e.g. see the list in embodiment 6), such as 2'-O-MOE nucleoside(s).
39. The single stranded antisense oligonucleotide according to any one of embodiments 1 to 38 wherein the antisense oligonucleotide comprises a region of 3 or more contiguous MOE nucleosides, and optionally wherein all the nucleosides of the oligonucleotide are 2'MOE nucleosides.
- 30 40. The single stranded antisense oligonucleotide according to any one of embodiments 1 – 39, wherein the target is a mRNA or a pre-mRNA target.

41. The single stranded antisense oligonucleotide according to any one of embodiments 1 – 40, wherein the oligonucleotide targets a pre-mRNA splice site or a region of the pre-mRNA which regulates the splicing event at a pre-mRNA splice site.
42. The single stranded antisense oligonucleotide according to any one of embodiments 1 – 41, which is a splice modulating oligonucleotide capable of modulating the splicing of a pre-mRNA target.
43. The single stranded antisense oligonucleotide according to any one of embodiments 1 – 42, wherein the target is a microRNA.
44. The single stranded antisense oligonucleotide according to any one of embodiments 1 – 42, wherein the antisense oligonucleotide is 10 – 20 nucleotides in length, such as 12 – 24 nucleotides in length.
45. The single stranded antisense oligonucleotide according to embodiment 43, wherein the length of the antisense oligonucleotide is 7 – 30, such as 8 – 12 or 12 to 23 nucleotides in length.
46. An single stranded antisense oligonucleotide comprising the antisense oligonucleotide according to any one of embodiments 1 – 45, wherein the oligonucleotide further comprises a 5' region position 5' to the contiguous nucleotide sequence, wherein the 5' nucleoside region comprises at least one phosphodiester linkage.
47. The single stranded antisense oligonucleotide according to embodiment 46, wherein the 5' region comprises 1 – 5 phosphodiester linked DNA nucleosides, and optionally may link the oligonucleotide or contiguous nucleotide sequence thereof to a conjugate moiety.
48. The single stranded antisense oligonucleotide according to any one of embodiments 1 to 47, wherein one or more nucleoside is a nucleobase modified nucleoside.
49. The single stranded antisense oligonucleotide according to any one of embodiments 1 to 48, wherein one or more nucleoside is 5-methyl cytosine, such as a LNA 5-methyl cytosine or a DNA 5-methyl cytosine.
50. A pharmaceutically acceptable salt of a single stranded antisense oligonucleotide according to any one of embodiments 1 to 49, in particular a sodium or a potassium salt or ammonium salt.
51. A conjugate comprising a single stranded antisense oligonucleotide, or a pharmaceutically acceptable salt according to any one of embodiments 1 to 49 and at

least one conjugate moiety covalently attached to said oligonucleotide or said pharmaceutically acceptable salt, optionally via a linker moiety.

52. A pharmaceutical composition comprising a single stranded antisense oligonucleotide, pharmaceutically acceptable salt or conjugate according to any one of embodiments 1 to 51 and a therapeutically inert carrier.
53. A single stranded antisense oligonucleotide, pharmaceutically acceptable salt or conjugate according to any one of embodiments 1 to 52 for use as a therapeutically active substance.
54. The single stranded antisense oligonucleotide, pharmaceutically acceptable salt or conjugate according to any one of embodiments 1 to 53 for use in therapy, for administration to a subject via parenteral administration, such as, intravenous, subcutaneous, intra-muscular, intracerebral, intracerebroventricular or intrathecal administration.
55. The in vitro use of a single stranded antisense oligonucleotide, salt, or composition according to any one of the preceding embodiments for use in the inhibition of a target RNA in a cell, wherein the single stranded antisense oligonucleotide is complementary to, such as fully complementary to the target RNA.
56. An in vivo or in vitro method for the inhibition of a target RNA in a cell which is expressing said target RNA, said method comprising administering an effective amount of the antisense oligonucleotide, salt, conjugate or composition according to any one of the preceding embodiments to the cell, so as to inhibit the target RNA.
57. The in vitro or in vivo use of a single stranded antisense oligonucleotide, salt, or composition according to any one of the preceding embodiments for use in the modulating the splicing of a target pre-mRNA in a cell.
58. An in vivo or in vitro method for modulating the splicing of a target pre-RNA in a cell which is expressing said target pre-RNA, said method comprising administering an effective amount of the antisense oligonucleotide, salt, conjugate or composition according to any one of the preceding embodiments to the cell, so as to modulate the splicing of the target RNA.

Htra-1 Targeting Antisense Oligonucleotides of the Invention

In some embodiments, the antisense oligonucleotide of the invention is complementary to the mRNA or pre-mRNA encoding the human high temperature requirement A1 Serine protease (Htra1) – see WO 2018/002105 for example. Inhibition of

Htra1 expression using the antisense oligonucleotides of the invention which target Htra1 mRNA or premRNA are beneficial for a treating a range of medical disorders, such as macular degeneration, e.g. age-related macular degeneration (geographic atrophy). Human Htra1 pre-mRNA and mRNA target sequences are available as follows:

Species	Chr	Strand	Genomic coordinates		Assembly	NCBI reference sequence* accession number for mRNA
			Start	End		
Human	10	fwd	12246152 5	12251490 8	GRCh38.p2 release 107	NM_002775.4

5 Compounds of the invention which target Htra-1 are listed as Htra1#1 – 38 in the examples.

1. An antisense oligonucleotide of the invention which is 10 – 30 nucleotides in length, wherein said antisense oligonucleotide targets the human HTRA1 mRNA or pre-mRNA, wherein said antisense oligonucleotide comprises a contiguous
 10 nucleotide region of 10 – 22 nucleotides which are at least 90% such as 100% complementarity to SEQ ID NO 1 or 2 of WO 2018/002105, which disclosed in the sequence listing as SEQ ID NO 9 and 10, wherein said antisense oligonucleotide comprises at least one phosphorodithioate internucleoside linkage of formula IA or formula IB.

15 2. The antisense oligonucleotide according to embodiment 1 or 2, wherein the contiguous nucleotide region is identical to a sequence present in a sequence selected from the group consisting of SEQ ID NO 11, 12, 13, 14, 15, 16, 17 and 18:

SEQ ID NO 11: CAAATATTTACCTGGTTG

SEQ ID NO 12: TTTACCTGGTTGTTGG

20 SEQ ID NO 13: CCAAATATTTACCTGGTT

SEQ ID NO 14: CCAAATATTTACCTGGTTGT

SEQ ID NO 15: ATATTTACCTGGTTGTTG

SEQ ID NO 16: TATTTACCTGGTTGTT

SEQ ID NO 17: ATATTTACCTGGTTGT

SEQ ID NO 18: ATATTTACCTGGTTGT

3. The antisense oligonucleotide according to any one of embodiments 1 - 3, wherein the contiguous nucleotide region comprises the sequence SEQ ID NO 146:
- 5 SEQ ID NO 19: TTTACCTGGTT
4. The antisense oligonucleotide according to any one of embodiments 1 - 4, wherein the contiguous nucleotide region of the oligonucleotide consists or comprises of a sequence selected from any one of SEQ ID NO 11, 12, 13, 14, 15, 16, 17 and 18.
- 10 5. The antisense oligonucleotide according to any one of embodiments 1 - 5 wherein the contiguous nucleotide region of the oligonucleotide comprises one or more 2' sugar modified nucleosides such as one or more 2' sugar modified nucleoside independently selected from the group consisting of 2'-O-alkyl-RNA, 2'-O-methyl-RNA, 2'-alkoxy-RNA, 2'-O-methoxyethyl-RNA, 2'-amino-DNA, 2'-fluoro-DNA, arabino nucleic acid (ANA), 2'-fluoro-ANA and LNA nucleosides.
- 15 6. The antisense oligonucleotide according to any one of embodiments 1 - 5, where the contiguous nucleotide region of the oligonucleotide comprises at least one modified internucleoside linkage, such as one or more phosphorothioate internucleoside linkages, or such as all the internucleoside linkages within the contiguous nucleotide region are phosphorothioate internucleoside linkages.
- 20 7. The antisense oligonucleotide according to any one of embodiments 1 - 6, wherein the oligonucleotide or contiguous nucleotide sequence thereof is or comprises a gapmer such as a gapmer of formula 5'-F-G-F'-3', where region F and F' independently comprise 1 - 7 sugar modified nucleosides and G is a region 6 - 16 nucleosides which is capable of recruiting RNaseH, wherein the nucleosides of regions F and F' which are adjacent to region G are sugar modified nucleosides.
- 25 8. The antisense oligonucleotide according to embodiment 7, wherein at least one of or both of region F and F' each comprise at least one LNA nucleoside.
9. The antisense oligonucleotide according to any one of embodiments 1 - 8, selected from the group selected from: Htra1#1 - 38, wherein a capital letter represents beta-D-oxy LNA nucleoside unit, a lower case letter represents a DNA nucleoside unit, subscript s represents a phosphorothioate internucleoside linkage, wherein all LNA cytosines are 5-methyl cytosine, P represents a phosphorodithioate internucleoside linkage of formula IB, S represents a Sp stereodefined phosphorothioate
- 30

internucleoside linkage, R represents a Rp stereodefined phosphorothioate internucleoside linkage, and X represents a stereorandom phosphorothioate linkage.

10. The antisense oligonucleotide according to any one of the previous embodiments in the form a salt, such as a sodium salt, a potassium salt or an ammonium salt (e.g. a pharmaceutically acceptable salt).
11. A conjugate comprising the oligonucleotide according to any one of embodiments 1 – 10, and at least one conjugate moiety covalently attached to said oligonucleotide, or salt thereof.
12. A pharmaceutical composition comprising the oligonucleotide of embodiment 1 – 10 or the conjugate of embodiment 11 and a pharmaceutically acceptable diluent, solvent, carrier, salt and/or adjuvant.
13. An in vivo or in vitro method for modulating HTRA1 expression in a target cell which is expressing HTRA1, said method comprising administering an oligonucleotide of any one of embodiments 1 – 10 or the conjugate according to embodiment 11 or the pharmaceutical composition of embodiment 12 in an effective amount to said cell.
14. A method for treating or preventing a disease comprising administering a therapeutically or prophylactically effective amount of an oligonucleotide of any one of embodiments 1 – 10 or the conjugate according to embodiment 11 or the pharmaceutical composition of embodiment 12 to a subject suffering from or susceptible to the disease.
15. The oligonucleotide of any one of embodiments 1 – 10 or the conjugate according to embodiment 11 or the pharmaceutical composition of embodiment 12 for use in medicine.
16. The oligonucleotide of any one of embodiments 1 – 10 or the conjugate according to embodiment 11 or the pharmaceutical composition of embodiment 12 for use in the treatment or prevention of a disease is selected from the group consisting of macular degeneration (such as wetAMD, dryAMD, geographic atrophy, intermediate dAMD, diabetic retinopathy), Parkinson's disease, Alzheimer's disease, Duchenne muscular dystrophy, arthritis, such as osteoarthritis, and familial ischemic cerebral small-vessel disease.
17. Use of the oligonucleotide of embodiment 1 – 10 or the conjugate according to embodiment 11 or the pharmaceutical composition of embodiment 12, for the preparation of a medicament for treatment or prevention of a disease is selected

from the group consisting of macular degeneration (such as wetAMD, dryAMD, geographic atrophy, intermediate dAMD, diabetic retinopathy), Parkinson's disease, Alzheimer's disease, Duchenne muscular dystrophy, arthritis, such as osteoarthritis, and familial ischemic cerebral small-vessel disease.

- 5 18. The oligonucleotide, conjugate, salt or composition or use according to any one of the preceding embodiments, for use in the treatment of geographic atrophy.

FURTHER EMBODIMENTS OF THE INVENTION

The invention thus relates in particular to:

- 10 An oligonucleotide according to the invention wherein the oligonucleotide is an antisense oligonucleotide capable of modulating the expression of a target RNA in a cell expressing said target RNA;

An oligonucleotide according to the invention wherein the oligonucleotide is an antisense oligonucleotide capable of inhibiting the expression of a target RNA in a cell expressing said target RNA;

- 15 An oligonucleotide according to the invention wherein one of (A¹) and (A²) is a LNA nucleoside and the other one is a DNA nucleoside, a RNA nucleoside or a sugar modified nucleoside;

An oligonucleotide according to the invention wherein one of (A¹) and (A²) is a LNA nucleoside and the other one is a DNA nucleoside or a sugar modified nucleoside;

- 20 An oligonucleotide according to the invention wherein one of (A¹) and (A²) is a LNA nucleoside and the other one is a DNA nucleoside;

An oligonucleotide according to the invention wherein one of (A¹) and (A²) is a LNA nucleoside and the other one is a sugar modified nucleoside;

- 25 An oligonucleotide according to the invention wherein said sugar modified nucleoside is a 2'-sugar modified nucleoside;

An oligonucleotide according to the invention wherein said 2'-sugar modified nucleoside is 2'-alkoxy-RNA, 2'-alkoxyalkoxy-RNA, 2'-amino-DNA, 2'-fluoro-RNA, 2'-fluoro-ANA or a LNA nucleoside;

- 30 An oligonucleotide according to the invention wherein said 2'-sugar modified nucleoside is a LNA nucleoside;

An oligonucleotide according to the invention wherein the LNA nucleosides are independently selected from beta-D-oxy LNA, 6'-methyl-beta- D-oxy LNA and ENA;

An oligonucleotide according to the invention wherein the LNA nucleosides are both beta-D-oxy LNA;

5 An oligonucleotide according to the invention wherein said 2'-sugar modified nucleoside is 2'-alkoxyalkoxy-RNA;

An oligonucleotide according to the invention wherein 2'-alkoxy-RNA is 2'-methoxy-RNA;

10 An oligonucleotide according to the invention wherein 2'-alkoxyalkoxy-RNA is 2'-methoxyethoxy-RNA;

An oligonucleotide according to the invention comprising between 1 and 15, in particular between 1 and 5, more particularly 1, 2, 3, 4 or 5 phosphorodithioate internucleoside linkages of formula (I) as defined above;

15 An oligonucleotide according to the invention comprising further internucleoside linkages independently selected from phosphodiester internucleoside linkage, phosphorothioate internucleoside linkage and phosphorodithioate internucleoside linkage of formula (I) as defined above;

20 An oligonucleotide according to the invention wherein the further internucleoside linkages are independently selected from phosphorothioate internucleoside linkage and phosphorodithioate internucleoside linkage of formula (I) as defined above.

An oligonucleotide according to the invention wherein the further internucleoside linkages are all phosphorothioate internucleoside linkages;

25 An oligonucleotide according to the invention wherein the further internucleoside linkages are all phosphorodithioate internucleoside linkages of formula (I) as defined above;

An oligonucleotide according to the invention wherein the oligonucleotide is a gapmer, in particular a LNA gapmer, a mixed wing gapmer, an alternating flank gapmer, a splice switching oligomer, a mixmer or a totalmer;

30 An oligonucleotide according to the invention which is a gapmer and wherein the at least one phosphorodithioate internucleoside linkage of formula (I) is comprised in the gap region and/or in one or more flanking region of the gapmer;

An oligonucleotide according to the invention where the contiguous nucleotide sequence, such as the gapmer region F-G-F', is flanked by flanking region D' or D'' or D' and D'', comprising one or more DNA nucleosides connected to the rest of the oligonucleotide through phosphodiester internucleoside linkages;

- 5 An oligonucleotide according to the invention which is a gapmer wherein one or both, particularly one, of the flanking regions F and F', are further flanked by phosphodiester linked DNA nucleosides, in particular 1 to 5 phosphodiester linked DNA nucleosides (region D' and D'');

- 10 An oligonucleotide according to the invention wherein the oligonucleotide is of 7 to 30 nucleotides in length.

When the oligonucleotide of the invention is a gapmer, it is advantageously of 12 to 26 nucleotides in length. 16 nucleotides is a particularly advantageous gapmer oligonucleotide length.

- 15 When the oligonucleotide is a full LNA oligonucleotide, it is advantageously of 7 to 10 nucleotides in length.

When the oligonucleotide is a mixmer oligonucleotide, it is advantageously of 8 to 30 nucleotides in length.

The invention relates in particular to:

- 20 An oligonucleotide according to the invention wherein one or more nucleoside is a nucleobase modified nucleoside;

An oligonucleotide according to the invention wherein the oligonucleotide is an antisense oligonucleotide, a siRNA, a microRNA mimic or a ribozyme;

A pharmaceutically acceptable salt of an oligonucleotide according to the invention, in particular a sodium or a potassium salt;

- 25 A conjugate comprising an oligonucleotide or a pharmaceutically acceptable salt according to the invention and at least one conjugate moiety covalently attached to said oligonucleotide or said pharmaceutically acceptable salt, optionally *via* a linker moiety;

A pharmaceutical composition comprising an oligonucleotide, pharmaceutically acceptable salt or conjugate according to the invention and a therapeutically inert carrier;

- 30 An oligonucleotide, pharmaceutically acceptable salt or conjugate according to the invention for use as a therapeutically active substance; and

The use of an oligonucleotide, pharmaceutically acceptable salt or conjugate according to the invention as a medicament;

In some embodiments, the oligonucleotide of the invention has a higher activity in modulating its target nucleic acid, as compared to the corresponding fully
5 phosphorothioate linked-oligonucleotide. In some embodiments the invention provides for oligonucleotides with enhanced activity, enhanced potency, enhanced specific activity or enhanced cellular uptake. In some embodiments the invention provides for oligonucleotides which have an altered duration of action *in vitro* or *in vivo*, such as a prolonged duration of action *in vitro* or *in vivo*. In some embodiments the higher activity
10 in modulating the target nucleic acid is determined *in vitro* or *in vivo* in a cell which is expressing the target nucleic acid.

In some embodiments the oligonucleotide of the invention has altered pharmacological properties, such as reduced toxicity, for example reduced nephrotoxicity, reduced hepatotoxicity or reduced immune stimulation. Hepatotoxicity may be
15 determined, for example *in vivo*, or by using the *in vitro* assays disclosed in WO 2017/067970, hereby incorporated by reference. Nephrotoxicity may be determined, for example *in vitro*, or by using the assays disclosed in PCT/EP2017/064770, hereby incorporated by reference. In some embodiments the oligonucleotide of the invention comprises a 5' CG 3' dinucleotide, such as a DNA 5' CG 3' dinucleotide, wherein the
20 internucleoside linkage between C and G is a phosphorodithioate internucleoside linkage of formula (I) as defined above.

In some embodiments, the oligonucleotide of the invention has improved nuclease resistance such as improved biostability in blood serum. In some embodiments, the 3' terminal nucleoside of the oligonucleotide of the invention has an A or G base, such as a
25 3' terminal LNA-A or LNA-G nucleoside. Suitably, the internucleoside linkage between the two 3' most nucleosides of the oligonucleotide may be a phosphorodithioate internucleoside linkage according to formula (I) as defined above.

In some embodiments the oligonucleotide of the invention has enhanced bioavailability. In some embodiments the oligonucleotide of the invention has a greater
30 blood exposure, such as a longer retention time in blood.

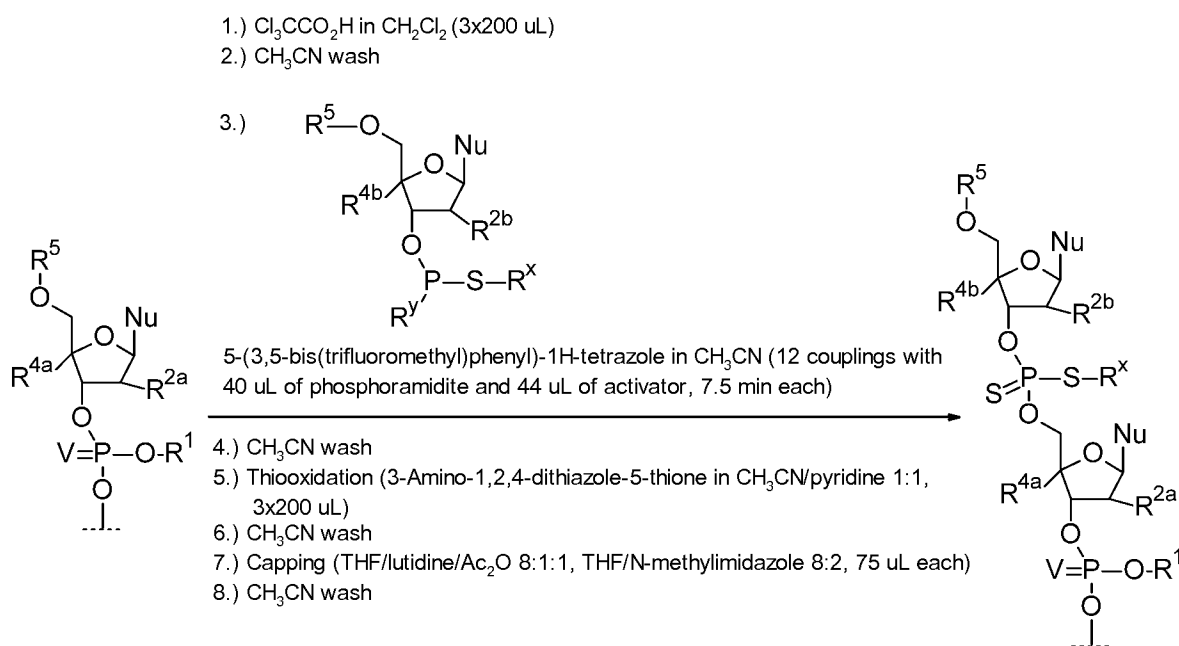
The non-bridging phosphorodithioate modification is introduced into oligonucleotides by means of solid phase synthesis using the phosphoramidite method. Syntheses are performed using controlled pore glass (CPG) equipped with a universal linker as the support. On such a solid support an oligonucleotide is typically built up in a
35 3' to 5' direction by means of sequential cycles consisting of coupling of 5'-O-DMT protected nucleoside phosphoramidite building blocks followed by (thio)oxidation,

capping and deprotection of the DMT group. Introduction of non-bridging phosphorodithioates is achieved using appropriate thiophosphoramidite building blocks followed by thiooxidation of the primary intermediate.

While the corresponding DNA thiophosphoramidites are commercially available, the
5 respective LNA building blocks have not been described before. They can be prepared
from the 5'-O-DMT-protected nucleoside 3'-alcohols e.g. by the reaction with mono-
benzoyl protected ethanedithiol and tripyrrolidin-1-ylphosphane.

The oligonucleotide according to the invention can thus for example be manufactured according to Scheme 2, wherein R¹, R^{2a}, R^{2b}, R^{4a}, R^{4b}, R⁵, R^x, R^y and V are
10 as defined below.

Scheme 2

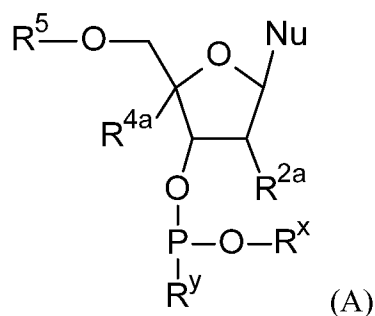


The invention thus also relates to a process for the manufacture of an oligonucleotide
15 according to the invention comprising the following steps:

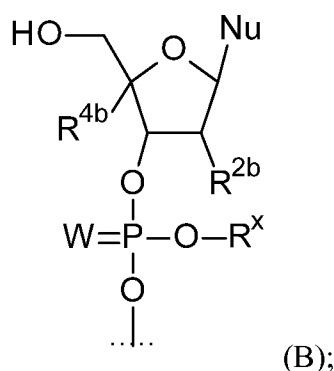
- (a) Coupling a thiophosphoramidite nucleoside to the terminal 5' oxygen atom of a nucleotide or oligonucleotide to produce a thiophosphite triester intermediate;
- (b) Thiooxidizing the thiophosphite triester intermediate obtained in step (a); and
- (c) Optionally further elongating the oligonucleotide.

20 The invention relates in particular to a process for the manufacture of an oligonucleotide according to the invention comprising the following steps:

(a1) Coupling a compound of formula (A)



to the 5' oxygen atom of a nucleotide or oligonucleotide of formula (B)



5 (b1) Thiooxidizing the thiophosphite triester intermediate obtained in step (a1); and

(c1) Optionally further elongating the oligonucleotide;

wherein

R^{2a} and R^{4a} together form -X-Y- as defined above; or

10 R^{4a} is hydrogen and R^{2a} is selected from alkoxy, in particular methoxy, halogen, in particular fluoro, alkoxyalkoxy, in particular methoxyethoxy, alkenyloxy, in particular allyloxy and aminoalkoxy, in particular aminoethyloxy;

R^{2b} and R^{4b} together form -X-Y- as defined above; or

R^{2b} and R^{4b} are both hydrogen at the same time; or

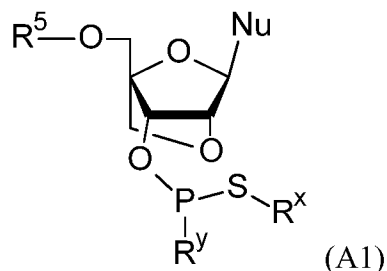
15 R^{4b} is hydrogen and R^{2b} is selected from alkoxy, in particular methoxy, halogen, in particular fluoro, alkoxyalkoxy, in particular methoxyethoxy, alkenyloxy, in particular allyloxy and aminoalkoxy, in particular aminoethyloxy;

V is oxygen or sulfur; and

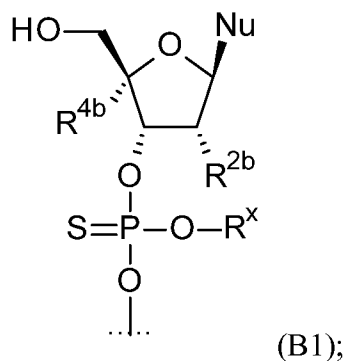
wherein R^5 , R^x , R^y and Nu are as defined below.

The invention relates in particular to a process for the manufacture of an oligonucleotide according to the invention comprising the following steps:

(a2) Coupling a compound of formula (II)



5 to the 5' oxygen atom of a nucleotide or oligonucleotide of formula (IV)



(b2) Thiooxidizing the thiophosphite triester intermediate obtained in step (a2); and

(c2) Optionally further elongating the oligonucleotide;

wherein

10 R^{2b} and R^{4b} together form -X-Y- as defined above; or

R^{2b} and R^{4b} are both hydrogen at the same time; or

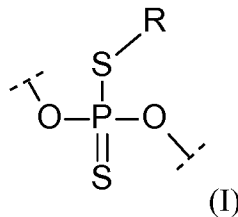
R^{4b} is hydrogen and R^{2b} is selected from alkoxy, in particular methoxy, halogen, in particular fluoro, alkoxyalkoxy, in particular methoxyethoxy, alkenyloxy, in particular allyloxy and aminoalkoxy, in particular aminoethyloxy; and

15 wherein R^5 , R^x , R^y and Nu are as defined below.

The invention also relates to an oligonucleotide manufactured according to a process of the invention.

The invention further relates to:

A gapmer oligonucleotide comprising at least one phosphorodithioate internucleoside linkage of formula (I)



wherein R is hydrogen or a phosphate protecting group;

- 5 A gapmer oligonucleotide as defined above wherein the oligonucleotide is an antisense oligonucleotide capable of modulating the expression of a target RNA in a cell expressing said target RNA;

- A gapmer oligonucleotide as defined above wherein the oligonucleotide is an antisense oligonucleotide capable of inhibiting the expression of a target RNA in a cell
10 expressing said target RNA;

A gapmer oligonucleotide as defined above capable of recruiting RNaseH, such as human RNaseH1;

- A gapmer oligonucleotide according to the invention wherein one of the two oxygen atoms of said at least one internucleoside linkage of formula (I) is linked to the 3' carbon atom of an adjacent nucleoside (A¹) and the other one is linked to the 5' carbon atom of another nucleoside (A²), wherein at least one of the two nucleosides (A¹) and (A²) is a 2'-sugar modified nucleoside;
15

A gapmer oligonucleotide according to the invention wherein one of (A¹) and (A²) is a 2'-sugar modified nucleoside and the other one is a DNA nucleoside;

- 20 A gapmer oligonucleotide according to the invention wherein (A¹) and (A²) are both a 2'-modified nucleoside at the same time;

A gapmer oligonucleotide according to the invention wherein (A¹) and (A²) are both a DNA nucleoside at the same time;

- A gapmer oligonucleotide according to the invention wherein the gapmer
25 oligonucleotide comprises a contiguous nucleotide sequence of formula 5'-F-G-F'-3', wherein G is a region of 5 to 18 nucleosides which is capable of recruiting RNaseH, and said region G is flanked 5' and 3' by flanking regions F and F' respectively, wherein regions F and F' independently comprise or consist of 1 to 7 2'-sugar modified nucleotides, wherein the nucleoside of region F which is adjacent to region G is a 2'-sugar

modified nucleoside and wherein the nucleoside of region F' which is adjacent to region G is a 2'-sugar modified nucleoside;

A gapmer oligonucleotide according to the invention wherein the 2'-sugar modified nucleosides are independently selected from 2'-alkoxy-RNA, 2'-alkoxyalkoxy-RNA, 2'-amino-DNA, 2'-fluoro-RNA, 2'-fluoro-ANA and LNA nucleosides;

A gapmer oligonucleotide according to the invention wherein 2'-alkoxyalkoxy-RNA is a 2'-methoxyethoxy-RNA (2'-O-MOE);

A gapmer oligonucleotide according to the invention wherein region F and region F' comprise or consist of 2'-methoxyethoxy-RNA nucleotides;

A gapmer oligonucleotide according to the invention, wherein both regions F and F' consist of 2'-methoxyethoxy-RNA nucleotides, such as a gapmer comprising the F-G-F' of formula [MOE]₃₋₈[DNA]₈₋₁₆[MOE]₃₋₈, for example [MOE]₅[DNA]₁₀[MOE]₅ – i.e. where region F and F' consist of five 2'-methoxyethoxy-RNA nucleotides each, and region G consists of 10 DNA nucleotides;

A gapmer oligonucleotide according to the invention wherein at least one or all of the 2'-sugar modified nucleosides in region F or region F', or in both regions F and F', are LNA nucleosides;

A gapmer oligonucleotide according to the invention wherein region F or region F', or both regions F and F', comprise at least one LNA nucleoside and at least one DNA nucleoside;

A gapmer oligonucleotide according to the invention wherein region F or region F', or both region F and F' comprise at least one LNA nucleoside and at least one non-LNA 2'-sugar modified nucleoside, such as at least one 2'-methoxyethoxy-RNA nucleoside;

A gapmer oligonucleotide according to the invention wherein the gap region comprises 5 to 16, in particular 8 to 16, more particularly 8, 9, 10, 11, 12, 13 or 14 contiguous DNA nucleosides;

A gapmer oligonucleotide according to the invention wherein region F and region F' are independently 1, 2, 3, 4, 5, 6, 7 or 8 nucleosides in length;

A gapmer oligonucleotide according to the invention wherein region F and region F' each indendently comprise 1, 2, 3 or 4 LNA nucleosides;

A gapmer oligonucleotide according to the invention wherein the LNA nucleosides are independently selected from beta-D-oxy LNA, 6'-methyl-beta-D-oxy LNA and ENA;

A gapmer oligonucleotide according to the invention wherein the LNA nucleosides are beta-D-oxy LNA;

A gapmer oligonucleotide according to the invention wherein the oligonucleotide, or contiguous nucleotide sequence thereof (F-G-F'), is of 10 to 30 nucleotides in length, in particular 12 to 22, more particularly of 14 to 20 oligonucleotides in length;

A gapmer oligonucleotide according to the invention wherein the gapmer oligonucleotide comprises a contiguous nucleotide sequence of formula 5'-D'-F-G-F'-D''-3', wherein F, G and F' are as defined in any one of claims 4 to 17 and wherein region D' and D'' each independently consist of 0 to 5 nucleotides, in particular 2, 3 or 4 nucleotides, in particular DNA nucleotides such as phosphodiester linked DNA nucleosides;

A gapmer oligonucleotide according to the invention wherein the gapmer oligonucleotide is capable of recruiting human RNaseH1;

A gapmer oligonucleotide according to the invention wherein said at least one phosphorodithioate internucleoside linkage of formula (I) as defined above is positioned between adjacent nucleosides in region F or region F', between region F and region G or between region G and region F';

A gapmer oligonucleotide according to the invention which further comprises phosphorothioate internucleoside linkages;

A gapmer oligonucleotide according to the invention wherein the internucleoside linkages between the nucleosides of region G are independently selected from phosphorothioate internucleoside linkages and phosphorodithioate internucleoside linkages of formula (I) as defined above;

A gapmer oligonucleotide according to the invention wherein the internucleoside linkages between the nucleosides of region G comprise 0, 1, 2 or 3 phosphorodithioate internucleoside linkages of formula (I) as defined above;

A gapmer oligonucleotide according to the invention wherein the remaining internucleoside linkages are independently selected from the group consisting of phosphorothioate, phosphodiester and phosphorodithioate internucleoside linkages of formula (I) as defined above;

A gapmer oligonucleotide according to the invention wherein the internucleoside linkages between the nucleosides of region F and the internucleoside linkages between the

nucleosides of region F' are independently selected from phosphorothioate and phosphorodithioate internucleoside linkages of formula (I) as defined above;

A gapmer oligonucleotide according to the invention wherein each flanking region F and F' independently comprise 1, 2, 3, 4, 5, 6 or 7 phosphorodithioate internucleoside linkages of formula (I) as defined above;

A gapmer oligonucleotide according to the invention wherein the flanking regions F and F' together or individually comprise 1, 2, 3, 4, 5 or 6 phosphorodithioate internucleoside linkages of formula (I) as defined above, or all the internucleoside linkages in region F and/or region F' are phosphordithioate internucleoside linkages of formula (I) as defined above;

A gapmer oligonucleotide according to the invention wherein the flanking regions F and F' together comprise 1, 2, 3 or 4 phosphorodithioate internucleoside linkages of formula (I) as defined above;

A gapmer oligonucleotide according to the invention wherein flanking regions F and F' each comprise 2 phosphorodithioate internucleoside linkages of formula (I) as defined above;

A gapmer oligonucleotide according to the invention wherein all the internucleoside linkages of flanking regions F and/or F' are phosphordithioate internucleoside linkages of formula (I) as defined above;

A gapmer oligonucleotide according to the invention wherein the gapmer oligonucleotide comprises at least one stereodefined internucleoside linkage, such as at least one stereodefined phosphorothioate internucleoside linkage;

A gapmer oligonucleotide according to the invention wherein the gap region comprises 1, 2, 3, 4 or 5 stereodefined phosphorothioate internucleoside linkages;

A gapmer oligonucleotide according to the invention wherein all the internucleoside linkages between the nucleosides of the gap region are stereodefined phosphorothioate internucleoside linkages;

A gapmer oligonucleotide according to the invention wherein the at least one phosphorodithioate internucleoside linkage of formula (I) as defined above is positioned between the nucleosides of region F, or between the nucleosides of region F', or between region F and region G, or between region G and region F', and the remaining internucleoside linkages within region F and F', between region F and region G and between region G and region F', are independently selected from stereodefined

phosphorothioate internucleoside linkages, stereorandom internucleoside linkages, phosphorodithioate internucleoside linkage of formula (I) and phosphodiester internucleoside linkages;

A gapmer oligonucleotide according to the invention wherein the at least one
5 phosphorodithioate internucleoside linkage of formula (I) as defined above is positioned between at least two adjacent nucleosides of region F, or between the two adjacent nucleosides of region F', or between region F and region G, or between region G and region F', and the remaining internucleoside linkages between the nucleotides of region F and F' are independently selected from phosphorothioate internucleoside linkages,
10 phosphorodithioate internucleoside linkage of formula (I) and phosphodiester internucleoside linkages. The phosphorothioate internucleoside linkages of region F and F' may be either stereorandom or stereodefined, or may be independently selected from stereorandom and stereodefined;

A gapmer oligonucleotide according to the invention wherein the at least one
15 phosphorodithioate internucleoside linkage of formula (I) as defined above is positioned between at least two adjacent nucleosides of region F, or between at least two adjacent nucleosides of region F', or between region F and region G, or between region G and region F', and the remaining internucleoside linkages between the nucleotides of region F and F' are independently selected from phosphorothioate internucleoside linkages, and
20 phosphorodithioate internucleoside linkages of formula (I). The phosphorothioate internucleoside linkages of region F and F' may be either stereorandom or stereodefined, or may be independently selected from stereorandom and stereodefined;

A gapmer oligonucleotide according to the invention wherein the at least one
phosphorodithioate internucleoside linkage of formula (I) as defined above is positioned
25 between at least two adjacent nucleosides of region F, or between at least two adjacent nucleosides of region F', or between region F and region G, or between region G and region F', and the remaining internucleoside linkages between the nucleotides of region F and F', between region F and region G and between region G and region F', are independently selected from phosphorothioate internucleoside linkages and
30 phosphorodithioate internucleoside linkage of formula (I); The phosphorothioate internucleoside linkages of region F and F' may be either stereorandom or stereodefined, or may be independently selected from stereorandom and stereodefined;

A gapmer oligonucleotide according to the invention wherein the at least one
phosphorodithioate internucleoside linkage of formula (I) as defined above is positioned
35 between at least two adjacent nucleosides of region F, or between at least two adjacent nucleosides of region F', or between region F and region G, or between region G and region F', and the remaining internucleoside linkages between the nucleotides of region F

and F' and between region F and region G and between region G and region F', are independently selected from stereodefined phosphorothioate internucleoside linkages and phosphorodithioate internucleoside linkage of formula (I);

A gapmer oligonucleotide according to the invention wherein the at least one
5 phosphorodithioate internucleoside linkage of formula (I) as defined above is positioned between at least two adjacent nucleosides of region F, or between at least two adjacent nucleosides of region F', or between region F and region G, or between region G and region F', and the remaining internucleoside linkages within region F and F', between
10 internucleoside linkages, which may be all stereorandom phosphorothioate internucleoside linkages, all stereodefined phosphorothioate internucleoside linkages, or may be independently selected from stereorandom and stereodefined phosphorothioate internucleoside linkages;

A gapmer oligonucleotide according to the invention wherein the remaining
15 internucleoside linkages within region F, within region F' or within both region F and region F' are all phosphorodithioate internucleoside linkages of formula (I) as defined above;

A gapmer oligonucleotide according to the invention wherein the internucleoside linkages between the nucleosides of region G comprise 0, 1, 2 or 3 phosphorodithioate
20 internucleoside linkages of formula (I) as defined above and the remaining internucleoside linkages within region G are independently selected from stereodefined phosphorothioate internucleoside linkages and stereorandom phosphorothioate internucleoside linkages;

A gapmer oligonucleotide according to the invention wherein the internucleoside linkages between the nucleosides of region G comprise 0, 1, 2 or 3 phosphorodithioate
25 internucleoside linkages of formula (I) as defined above and at least one of the remaining internucleoside linkages within region G, or all of the remaining internucleoside linkages within region G are stereodefined phosphorothioate internucleoside linkages;

A gapmer oligonucleotide according to the invention wherein the internucleoside linkages between the nucleosides of region G comprise 0, 1, 2 or 3 phosphorodithioate
30 internucleoside linkages of formula (I) as defined above and the remaining internucleoside linkages within region G are phosphorothioate internucleoside linkages, such as stereorandom phosphorothioate internucleoside linkages;

A gapmer oligonucleotide according to the invention wherein at least one of region F or F' comprise the at least one phosphorodithioate internucleoside linkages of formula (I)

as defined above and all the internucleoside linkages within region G are phosphorothioate internucleoside linkages, such as stereorandom phosphorothioate internucleoside linkages;

A gapmer oligonucleotide according to the invention wherein at least one of region F or F' comprise the at least one phosphorodithioate internucleoside linkages of formula (I)
5 as defined above and all the internucleoside linkages within region G are phosphorothioate internucleoside linkages, wherein at least one of the phosphorothioate internucleoside linkages within region G is a stereodefined phosphorothioate internucleoside linkage;

A gapmer oligonucleotide according to the invention wherein at least one of region F or F' comprise the at least one phosphorodithioate internucleoside linkages of formula (I)
10 as defined above and all the internucleoside linkages within region G are stereodefined phosphorothioate internucleoside linkages;

A gapmer oligonucleotide according to the invention wherein the internucleoside linkage between region F and G, or the internucleoside linkage between region G and F', or both the internucleoside linkages between region F and G and between region G and F',
15 are phosphorodithioate internucleoside linkages of formula (I) as defined above, and wherein, in the event that only one of the internucleoside linkages between region F and G and between region G and F' is a phosphorodithioate internucleoside linkages of formula (I) as defined above, the other internucleoside linkage between region F and G or between region G and F' is a phosphorothioate internucleoside linkage;

A gapmer oligonucleotide according to the invention wherein at least one of region F or F' comprise the at least one phosphorodithioate internucleoside linkage of formula (I) as defined above, wherein the internucleoside linkage between region F and G, or the internucleoside linkage between region G and F', or both the internucleoside linkages between region F and G and between region G and F', are phosphorodithioate
20 internucleoside linkages of formula (I) as defined above and wherein in the event that only one of the internucleoside linkages between region F and G and between region G and F' is a phosphorodithioate internucleoside linkages of formula (I) as defined above, the other internucleoside linkage between region F and G or between region G and F' is a phosphorothioate internucleoside linkage;

A gapmer oligonucleotide according to the invention wherein the internucleoside linkages between the nucleosides of region G comprise 0, 1, 2 or 3 phosphorodithioate internucleoside linkages of formula (I) as defined above and the remaining internucleoside linkages within region G are phosphorothioate internucleoside linkages, wherein the internucleoside linkage between region F and G, or the internucleoside linkage between
30 region G and F', or both the internucleoside linkages between region F and G and between region G and F', are phosphorodithioate internucleoside linkages of formula (I) as defined

above and wherein in the event that only one of the internucleoside linkages between region F and G and between region G and F' is a phosphorodithioate internucleoside linkages of formula (I) as defined above, the other internucleoside linkage between region F and G or between region G and F' is a phosphorothioate internucleoside linkage;

- 5 A gapmer oligonucleotide according to the invention wherein at least one of region F or F' comprise the at least one phosphorodithioate internucleoside linkages of formula (I) as defined above, wherein the internucleoside linkages between the nucleosides of region G comprise 0, 1, 2 or 3 phosphorodithioate internucleoside linkages of formula (I) as defined above and the remaining internucleoside linkages within region G are
- 10 phosphorothioate internucleoside linkages, wherein the internucleoside linkage between region F and G, or the internucleoside linkage between region G and F', or both the internucleoside linkages between region F and G and between region G and F', are phosphorodithioate internucleoside linkages of formula (I) as defined above, and wherein, in the event that only one of the internucleoside linkages between region F and G and
- 15 between region G and F' is a phosphorodithioate internucleoside linkage of formula (I) as defined above, the other internucleoside linkage between region F and G or between region G and F' is a phosphorothioate internucleoside linkage;

- A gapmer oligonucleotide according to the invention wherein region F or region F' comprise at least one phosphorodithioate internucleoside linkages of formula (I) as defined
- 20 above, or wherein the internucleoside linkage between region F and region G, or between region G and region F' comprise at least one phosphorodithioate internucleoside linkage of formula (I) as defined above, region G comprises 1, 2 or 3 phosphorodithioate internucleoside linkages of formula (I) as defined above, and the remaining internucleoside linkages within region G are phosphorothioate internucleoside linkages;

- 25 A gapmer oligonucleotide according to the invention wherein region F or region F' comprise at least one phosphorodithioate internucleoside linkages of formula (I) as defined above, or wherein the internucleoside linkage between region F and region G, or between region G and region F' comprise at least one phosphorodithioate internucleoside linkages of formula (I) as defined above, all of the internucleoside linkage within region G are
- 30 phosphorothioate internucleoside linkages and wherein at least one of the phosphorothioate internucleoside linkages within region G is a stereodefined phosphorothioate internucleoside linkage;

- A gapmer oligonucleotide according to the invention wherein region F or region F' comprise at least one phosphorodithioate internucleoside linkages of formula (I) as defined
- 35 above, or wherein the internucleoside linkage between region F and region G, or between region G and region F' comprise at least one phosphorodithioate internucleoside linkages of formula (I) as defined above, all of the internucleoside linkages within region G are

phosphorothioate internucleoside linkages and wherein all of the phosphorothioate internucleoside linkages within region G are stereodefined phosphorothioate internucleoside linkages;

5 A gapmer oligonucleotide according to the invention wherein other than the at least one phosphorodithioate internucleoside linkages of formula (I) as defined above, all the remaining internucleoside linkages within the gapmer region F-G-F' are phosphorothioate internucleoside linkages;

10 A gapmer oligonucleotide according to the invention wherein at least one of region F or F' comprise the at least one phosphorodithioate internucleoside linkages of formula (I) as defined above and all the internucleoside linkages within region G are stereodefined phosphorothioate internucleoside linkages;

15 A gapmer oligonucleotide according to the invention wherein other than the at least one phosphorodithioate internucleoside linkages of formula (I) all the remaining internucleoside linkages within the gapmer region F-G-F' are stereodefined phosphorothioate internucleoside linkages;

A gapmer oligonucleotide according to the invention which is LNA gapmer, a mixed wing gapmer, an alternating flank gapmer or a gap-breaker gapmer.

A pharmaceutically acceptable salt of a gapmer oligonucleotide according to the invention, in particular a sodium or a potassium salt;

20 A conjugate comprising a gapmer oligonucleotide or a pharmaceutically acceptable salt according to the invention and at least one conjugate moiety covalently attached to said oligonucleotide or said pharmaceutically acceptable salt, optionally *via* a linker moiety, in particular *via* a biocleavable linker, particularly *via* 2 to 4 phosphodiester linked DNA nucleosides (e.g. region D' or D'');

25 A pharmaceutical composition comprising a gapmer oligonucleotide, pharmaceutically acceptable salt or conjugate according to the invention and a therapeutically inert carrier;

A gapmer oligonucleotide, pharmaceutically acceptable salt or conjugate according to the invention for use as a therapeutically active substance;

30 The use of a gapmer oligonucleotide, pharmaceutically acceptable salt or conjugate as a medicament;

A method of modulating the expression of a target RNA in a cell comprising administering an oligonucleotide or gapmer oligonucleotide according to the invention to a cell expressing said target RNA so as to modulate the expression of said target RNA;

- 5 A method of inhibiting the expression of target RNA in a cell comprising administering an oligonucleotide or gapmer oligonucleotide according to the invention to a cell expressing said target RNA so as to inhibit the expression of said target RNA; and

An *in vitro* method of modulating or inhibiting a target RNA in a cell comprising administering an oligonucleotide or gapmer oligonucleotide according to the invention to a cell expressing said target RNA, so as to modulate or inhibit said target RNA in said cell.

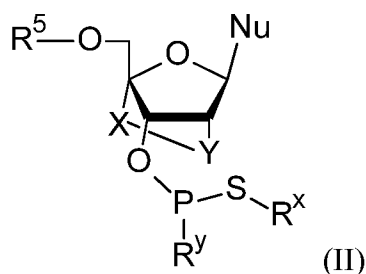
- 10 The target RNA can, for example be a mammalian mRNA, such as a pre-mRNA or mature mRNA, a human mRNA, a viral RNA or a non-coding RNA, such as a microRNA or a long non coding RNA.

In some embodiments, modulation is splice modulation of a pre-mRNA resulting in an altered splicing pattern of the target pre-mRNA.

- 15 In some embodiments, the modulation is inhibition which may occur via target degradation (*e.g.* via recruitment of RNaseH, such as RNaseH1 or RISC), or the inhibition may occur via an occupancy mediate mechanism which inhibits the normal biological function of the target RNA (*e.g.* mixmer or totalmer inhibition of microRNAs or long non coding RNAs).

- 20 The human mRNA can be a mature RNA or a pre-mRNA.

The invention also further relates to a compound of formula (II)



wherein

- 25 X is oxygen, sulfur, $-\text{CR}^a\text{R}^b-$, $-\text{C}(\text{R}^a)=\text{C}(\text{R}^b)-$, $-\text{C}(=\text{CR}^a\text{R}^b)-$, $-\text{C}(\text{R}^a)=\text{N}-$, $-\text{Si}(\text{R}^a)_2-$, $-\text{SO}_2-$, $-\text{NR}^a-$, $-\text{O}-\text{NR}^a-$, $-\text{NR}^a-\text{O}-$, $-\text{C}(=\text{J})-$, Se, $-\text{O}-\text{NR}^a-$, $-\text{NR}^a-\text{CR}^a\text{R}^b-$, $-\text{N}(\text{R}^a)-\text{O}-$ or $-\text{O}-\text{CR}^a\text{R}^b-$;

Y is oxygen, sulfur, $-(CR^aR^b)_n-$, $-CR^aR^b-O-CR^aR^b-$, $-C(R^a)=C(R^b)-$, $-C(R^a)=N-$, $-Si(R^a)_2-$, $-SO_2-$, $-NR^a-$, $-C(=J)-$, Se, $-O-NR^a-$, $-NR^a-CR^aR^b-$, $-N(R^a)-O-$ or $-O-CR^aR^b-$;

5 with the proviso that $-X-Y-$ is not $-O-O-$, $Si(R^a)_2-Si(R^a)_2-$, $-SO_2-SO_2-$, $-C(R^a)=C(R^b)-C(R^a)=C(R^b)-$, $-C(R^a)=N-C(R^a)=N-$, $-C(R^a)=N-C(R^a)=C(R^b)-$, $-C(R^a)=C(R^b)-C(R^a)=N-$ or $-Se-Se-$;

J is oxygen, sulfur, $=CH_2$ or $=N(R^a)$;

10 R^a and R^b are independently selected from hydrogen, halogen, hydroxyl, cyano, thiohydroxyl, alkyl, substituted alkyl, alkenyl, substituted alkenyl, alkynyl, substituted alkynyl, alkoxy, substituted alkoxy, alkoxyalkyl, alkenyloxy, carboxyl, alkoxycarbonyl, alkylcarbonyl, formyl, aryl, heterocyclyl, amino, alkylamino, carbamoyl, alkylaminocarbonyl, aminoalkylaminocarbonyl, alkylaminoalkylaminocarbonyl, alkylcarbonylamino, carbamido, alkanoyloxy, sulfonyl, alkylsulfonyloxy, nitro, azido, thiohydroxylsulfidealkylsulfanyl, 15 aryloxycarbonyl, aryloxy, arylcarbonyl, heteroaryl, heteroaryloxycarbonyl, heteroaryloxy, heteroarylcarbonyl, $-OC(=X^a)R^c$, $-OC(=X^a)NR^cR^d$ and $-NR^cC(=X^a)NR^cR^d$;

or two geminal R^a and R^b together form optionally substituted methylene;

20 or two geminal R^a and R^b , together with the carbon atom to which they are attached, form cycloalkyl or halocycloalkyl, with only one carbon atom of $-X-Y-$;

wherein substituted alkyl, substituted alkenyl, substituted alkynyl, substituted alkoxy and substituted methylene are alkyl, alkenyl, alkynyl and methylene substituted with 1 to 3 substituents independently selected from halogen, hydroxyl, alkyl, alkenyl, alkynyl, alkoxy, alkoxyalkyl, alkenyloxy, carboxyl, 25 alkoxycarbonyl, alkylcarbonyl, formyl, heterocyl, aryl and heteroaryl;

X^a is oxygen, sulfur or $-NR^c$;

R^c , R^d and R^e are independently selected from hydrogen and alkyl;

n is 1, 2 or 3.

R^5 is a hydroxyl protecting group;

30 R^x is phenyl, nitrophenyl, phenylalkyl, halophenylalkyl, cyanoalkyl, phenylcarbonylsulfanylalkyl, halophenylcarbonylsulfanylalkyl, alkylcarbonylsulfanylalkyl or alkylcarbonylcarbonylsulfanylalkyl;

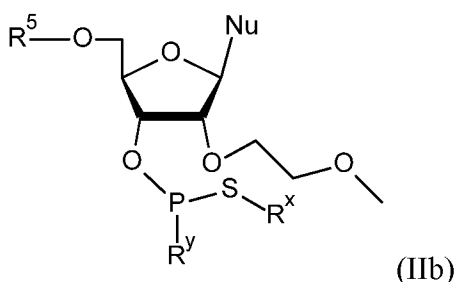
R^y is dialkylamino or pyrrolidinyl; and

Nu is a nucleobase or a protected nucleobase.

The invention further relates to:

A compound of formula (II) wherein -X-Y- is -CH₂-O-, -CH(CH₃)-O- or -CH₂CH₂-O-;

The invention further provides a compound of formula (IIb)



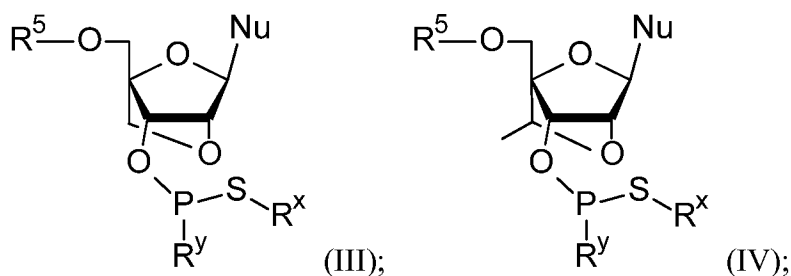
wherein R^5 is a hydroxyl protecting group,

R^x is phenyl, nitrophenyl, phenylalkyl, halophenylalkyl, cyanoalkyl, phenylcarbonylsulfanylalkyl, halophenylcarbonylsulfanylalkyl, alkylcarbonylsulfanylalkyl or alkylcarbonylcarbonylsulfanylalkyl;

R^y is dialkylamino or pyrrolidinyl; and

Nu is a nucleobase or a protected nucleobase;

A compound of formula (II) which is of formula (III) or (IV)



wherein R^5 , R^x , R^y and Nu are as above;

A compound of formula (II), (IIb), (III) or (IV) wherein R^x is phenyl, nitrophenyl, phenylmethyl, dichlorophenylmethyl, cyanoethyl, methylcarbonylsulfanylethyl, ethylcarbonylsulfanylethyl, isopropylcarbonylsulfanylethyl, tert.-butylcarbonylsulfanylethyl, methylcarbonylcarbonylsulfanylethyl or difluorophenylcarbonylsulfanylethyl;

- A compound of formula (II), (IIb), (III) or (IV) wherein R^x is phenyl, 4-nitrophenyl, 2,4-dichlorophenylmethyl, cyanoethyl, methylcarbonylsulfanylethyl, ethylcarbonylsulfanylethyl, isopropylcarbonylsulfanyethyl, tert.-butylcarbonylsulfanylethyl, methylcarbonylcarbonylsulfanylethyl or 2,4-difluorophenylcarbonylsulfanylethyl;

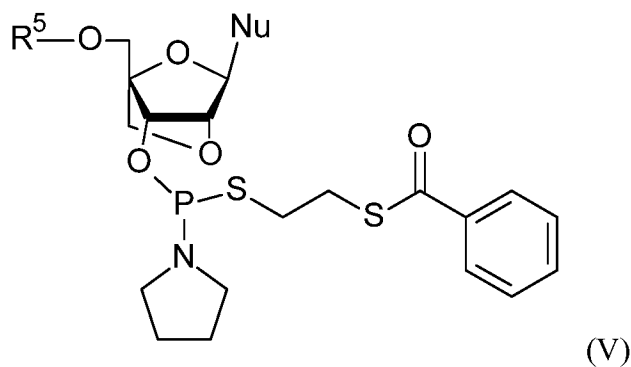
A compound of formula (II), (IIb), (III) or (IV) wherein R^x is phenylcarbonylsulfanylalkyl;

A compound of formula (II), (IIb), (III) or (IV) wherein R^x is phenylcarbonylsulfanylethyl;

- 10 A compound of formula (II), (IIb), (III) or (IV) wherein R^y is diisopropylamino or pyrrolidinyl;

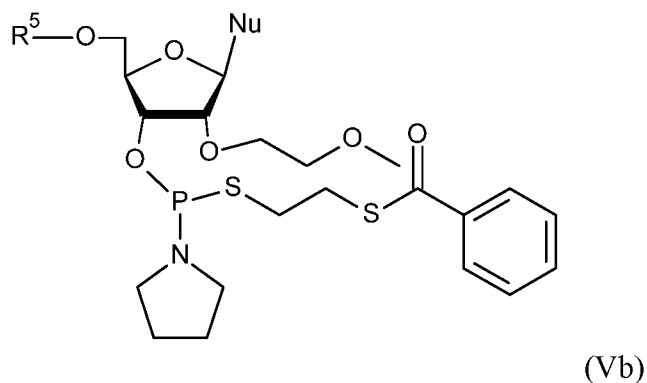
A compound of formula (II), (IIb), (III) or (IV) wherein R^y is pyrrolidinyl;

A compound of formula (II) which is of formula (V)



- 15 wherein R^5 and Nu are as defined above;

A compound of formula (IIb) which is of formula (Vb)



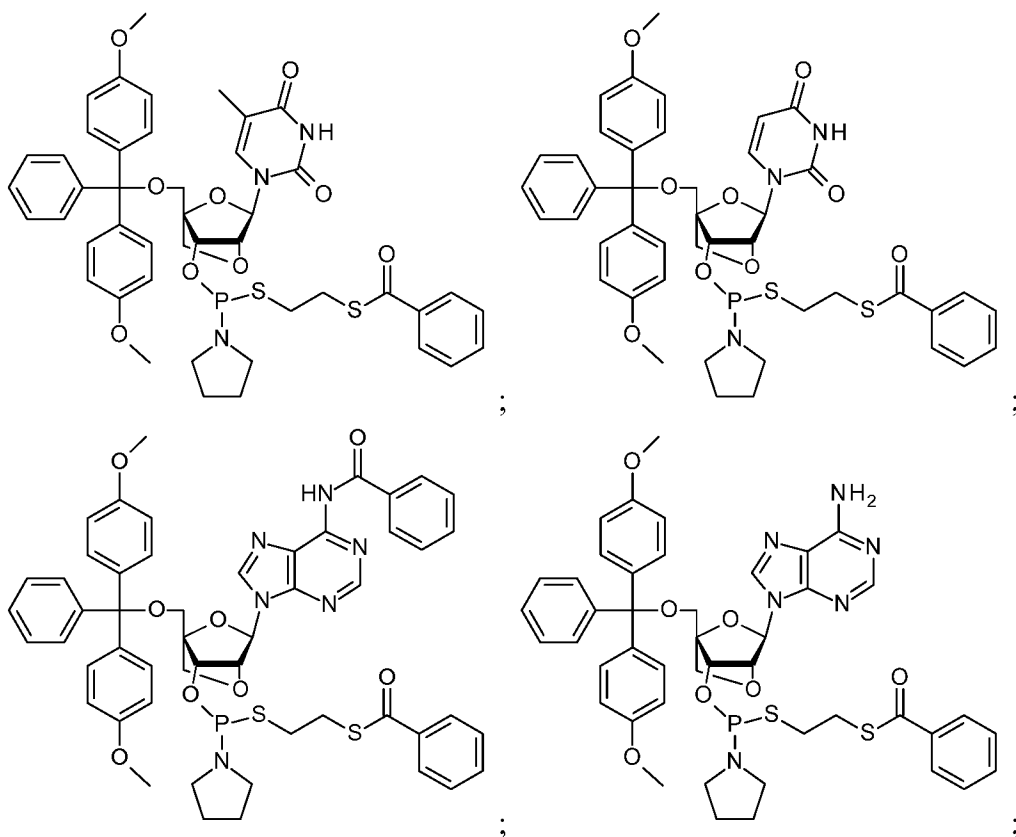
wherein R^5 and Nu are as defined above;

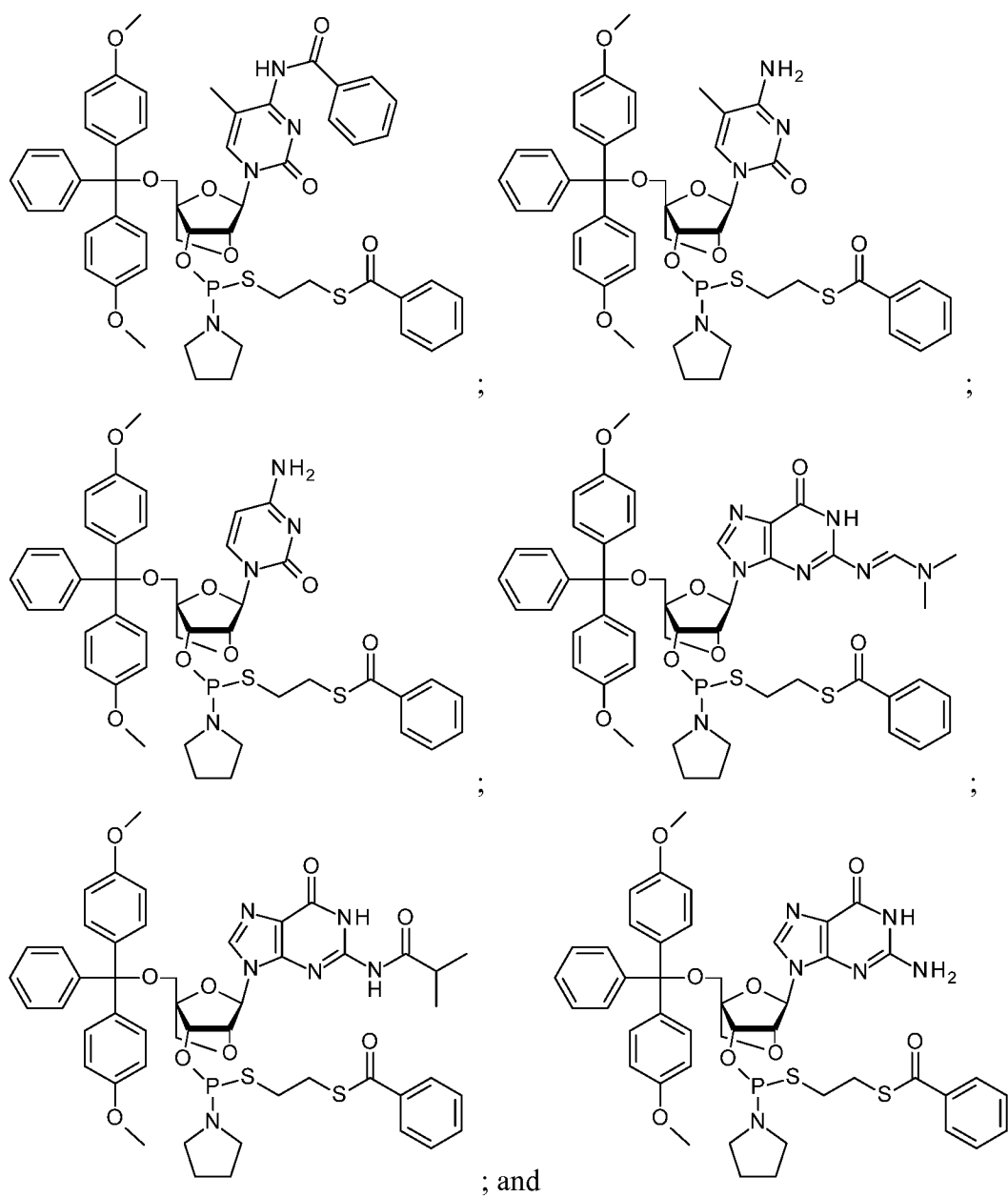
A compound of formula (II), (IIb), (III), (IV) or (V) or (Vb) wherein Nu is thymine, protected thymine, adenosine, protected adenosine, cytosine, protected cytosine, 5-methylcytosine, protected 5-methylcytosine, guanine, protected guanine, uracyl or protected uracyl;

- 5 A compound of formula (IIb) wherein Nu is thymine, protected thymine, adenosine, protected adenosine, cytosine, protected cytosine, 5-methylcytosine, protected 5-methylcytosine, guanine, protected guanine, uracyl or protected uracyl;

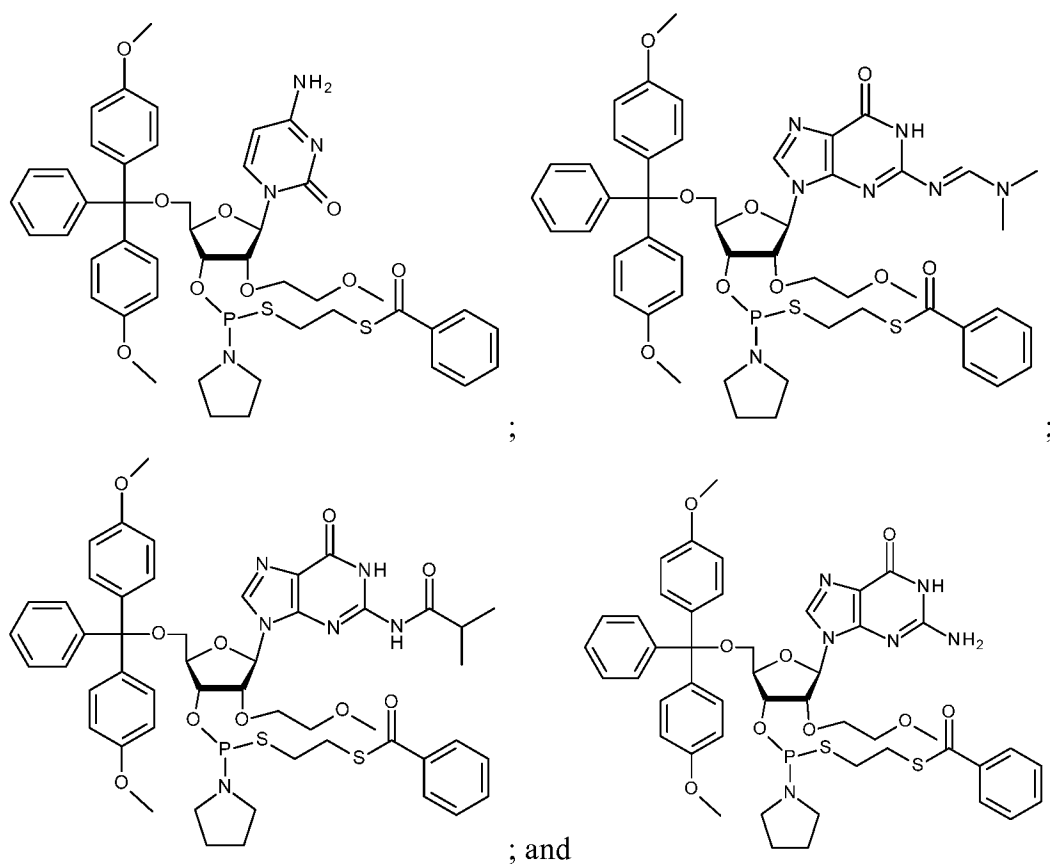
- A compound of formula (Vb) wherein Nu is thymine, protected thymine, adenosine, protected adenosine, cytosine, protected cytosine, 5-methylcytosine, protected 5-methylcytosine, guanine, protected guanine, uracyl or protected uracyl;
- 10

A compound of formula (II) selected from



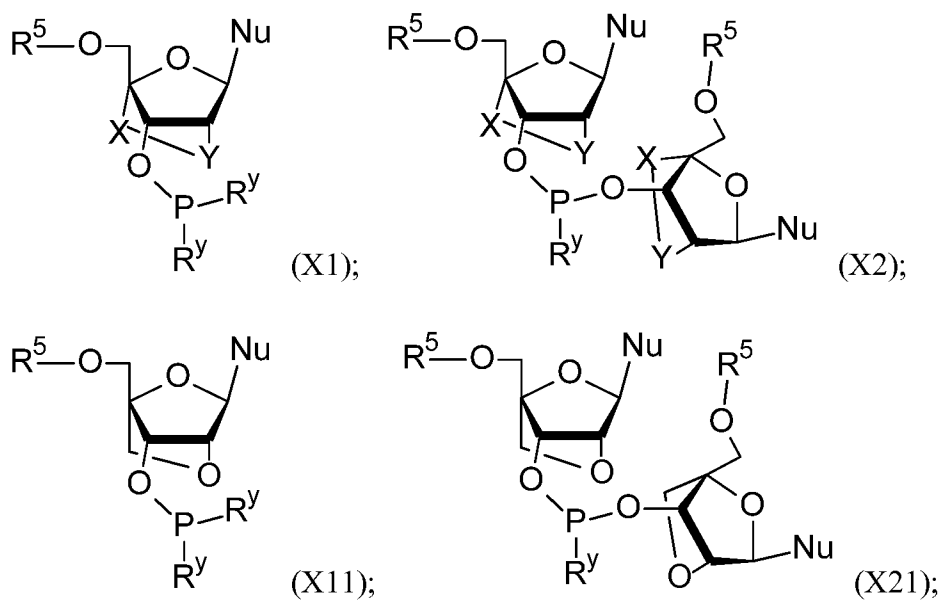


A compound of formula (IIb) selected from



- 5 The presence of impurities in the compound of formula (II) and (IIb) results in byproducts during the manufacture of oligonucleotides and hampers the success of the synthesis. Furthermore, in the presence of impurities, the compound of formula (II) or (IIb) is unstable on storage.

The compounds of formula (X1), (X2), X(11) and (X21)



are, among others, examples of such impurities.

There was thus the need for a compound of formula (II) or (IIb) in a sufficiently pure form for storage and oligonucleotide manufacture purposes.

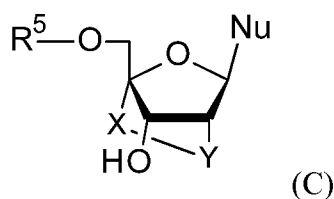
The invention thus also relates to a compound of formula (II) (IIb) having a purity of
5 at least 98 %, particularly of 99 %, more particularly of 100 %.

The invention thus relates in particular to a compound of formula (II) comprising less than 1 %, particularly 0 %, of the compound of formula (X1) and/or of the compound of (X2) as impurities.

The invention further relates to a process for the manufacture of a compound of
10 formula (II) as defined above comprising the reaction of a 5'-protected LNA nucleoside with a phosphine and a mono-protected dithiol in the presence of an acidic coupling agent and a silylation agent.

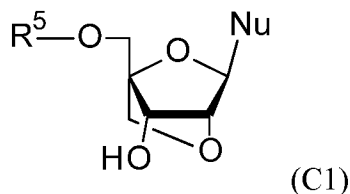
The invention further relates to a process for the manufacture of a compound of formula (IIb) as defined above comprising the reaction of a 5'-protected MOE nucleoside
15 with a phosphine and a mono-protected dithiol in the presence of an acidic coupling agent and a silylation agent.

The invention relates to a process for the manufacture of a compound of formula (II) comprising the reaction of a compound of formula (C)



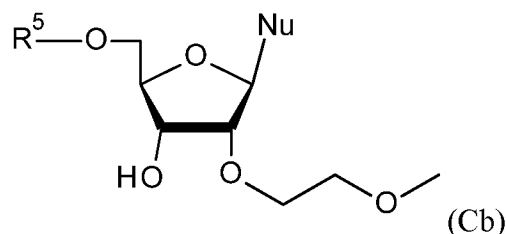
20 with a compound of formula $P(R^y)_3$ and a compound of formula HSR^x in the presence of an acidic coupling agent and a silylation agent, wherein X, Y, R^5 , Nu, R^x and R^y are as defined above.

The invention further relates to a process for the manufacture of a compound of formula (II) comprising the reaction of a compound of formula (C1)



with a compound of formula $P(R^y)_3$ and a compound of formula HSR^x in the presence of an acidic coupling agent and a silylation agent, wherein R^5 , Nu, R^x and R^y are as defined above.

- The invention also relates to a process for the manufacture of a compound of
 5 formula (IIb) comprising the reaction of a compound of formula (Cb)



with a compound of formula $P(R^y)_3$ and a compound of formula HSR^x in the presence of an acidic coupling agent and a silylation agent, wherein R^5 , Nu, R^x and R^y are as defined above.

- 10 Examples of acidic coupling agents, also known as acidic activator, are azole based activators like tetrazole, 5-nitrophenyl-1H-tetrazole (NPT), 5-ethylthio-1H-tetrazole (ETT), 5-benzylthio-1H-tetrazole (BTT), 5-methylthio-1H-tetrazole (MTT), 5-mercapto-
 tetrazoles (MCT), 5-(3,5-bis(trifluoromethyl)phenyl)-1H-tetrazole and 4,5-
 dicyanoimidazole (DCI), or acidic salts like pyridinium hydrochloride, imidazolium
 15 triflate, benzimidazolium triflate, 5-nitrobenzimidazolium triflate, or weak acids such as 2,4-dinitrobenzoic acid or 2,4-dinitrophenol. Tetrazole is a particular acidic coupling agents.

- Examples of silylation agents, also known as hydroxyl group quenchers, are
 bis(dimethylamino)dimethylsilane, N,O-bis(trimethylsilyl)acetamide (BSA), N,O-
 20 bis(trimethylsilyl)carbamate (BSC), N,N-bis(trimethylsilyl)methylamine, N,O-
 bis(trimethylsilyl)trifluoroacetamide (BSTFA), N,N'-bis(trimethylsilyl)urea (BSU),
 bromotrimethylsilane (TMBS), N-tert-butyldimethylsilyl-N-methyltrifluoroacetamide (MTBSTFA), chlorodimethyl(pentafluorophenyl)silane, chlorotriethylsilane (TESCI),
 chlorotrimethylsilane (TMCS), 1,3-dimethyl-1,1,3,3-tetraphenyldisilazane (TPDMDS),
 25 N,N-dimethyltrimethylsilylamine (TMSDMA), hexamethyldisilazane (HMDS),
 hexamethyldisiloxane (HMDSO), N-methyl-N-trimethylsilylacetamide (MSA), N-methyl-
 N-trimethylsilylheptafluorobutyramide (MSHFA), N-methyl-N-
 (trimethylsilyl)trifluoroacetamide (MSTFA), 1,1,3,3-tetramethyl-1,3-diphenyldisilazane
 (DPTMDS), 4-(trimethylsiloxy)-3-penten-2-one (TMS acac), 1-(trimethylsilyl)imidazole
 30 (TMSI) or trimethylsilyl methallylsulfinate (SILMAS-TMS). 1-(Trimethylsilyl)imidazole
 is a particular silylation agent.

The invention further relates to a process for the manufacture of a compound of formula (II), (IIb) or (III) wherein the crude compound of formula (II) or (IIb) is purified by preparative HPLC.

- 5 The invention further relates to a process for the manufacture of a compound of formula (II), (IIb) or (III) wherein the crude compound of formula (II), (IIb) or (III) is purified by preparative HPLC and eluted with a gradient of acetonitrile versus ammonium hydroxide in water.

- 10 The ammonium hydroxide content in water is in particular at least around 0.05 % v/v, in particular between around 0.05 % and 1 % v/v, more particularly between around 0.05 % and 0.5 % v/v, more particularly around 0.05 % v/v.

The gradient of acetonitrile is in particular between 0 % and 25 % to between 75 % and 100 % acetonitrile, in particular within 20 min to 120 min, more particularly between 10 % and 20 % to between 75 % and 90 % acetonitrile, in particular within 25 min to 60 min, more particularly around 25 % to 75 % acetonitrile, in particular within 30 min.

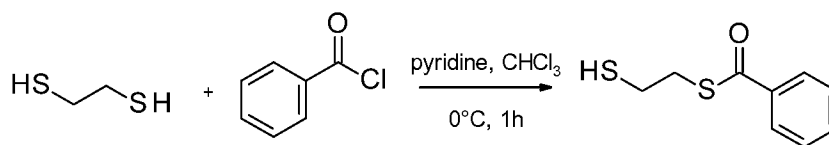
- 15 The invention also relates to the use of a compound of formula (II), (IIb) or (III) in the manufacture of an oligonucleotide, in particular of an oligonucleotide or a gapmer oligonucleotide according to the invention.

The invention will now be illustrated by the following examples which have no limiting character.

Examples

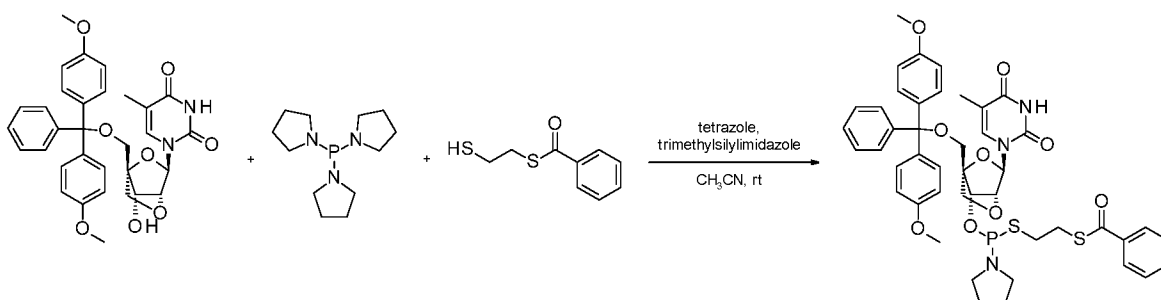
Example 1: Monomer synthesis

1.1: S-(2-sulfanylethyl) benzenecarbothioate



- 5 To a solution of 1,2-ethanedithiol (133.57 mL, 1592 mmol, 1 eq) and pyridine (64.4 mL, 796 mmol, 0.5 eq) in chloroform (200 mL) was added benzoyl chloride (92.4 mL, 796 mmol, 0.5 eq) in chloroform (200 mL) dropwise for 1 hr, and the reaction was stirred at 0 °C for 1 hr. The mixture was washed with water (300 mL) and brine (300 mL). The organic phase was dried over Na₂SO₄ and concentrated to a yellow oil. The oil was
- 10 distilled (135~145°C) to afford S-(2-sulfanylethyl) benzenecarbothioate (40 g, 202mmol, 13% yield) as a colorless oil. ¹H NMR (400 MHz, CDCl₃) δ 7.97 (d, *J*=7.34 Hz, 2H), 7.53-7.64 (m, 1H), 7.47 (t, *J*=7.58 Hz, 2H), 3.31 (t, *J*=7.34 Hz, 2H), 2.77-2.86 (m, 2H), 1.70 (t, *J*=8.56 Hz, 1H).

- 15 **1.2: S-[2-[[[(1R,3R,4R,7S)-1-[[bis(4-methoxyphenyl)-phenyl-methoxy]methyl]-3-(5-methyl-2,4-dioxo-pyrimidin-1-yl)-2,5-dioxabicyclo[2.2.1]heptan-7-yl]oxy-pyrrolidin-1-yl-phosphanyl]sulfanylethyl] benzenecarbothioate**

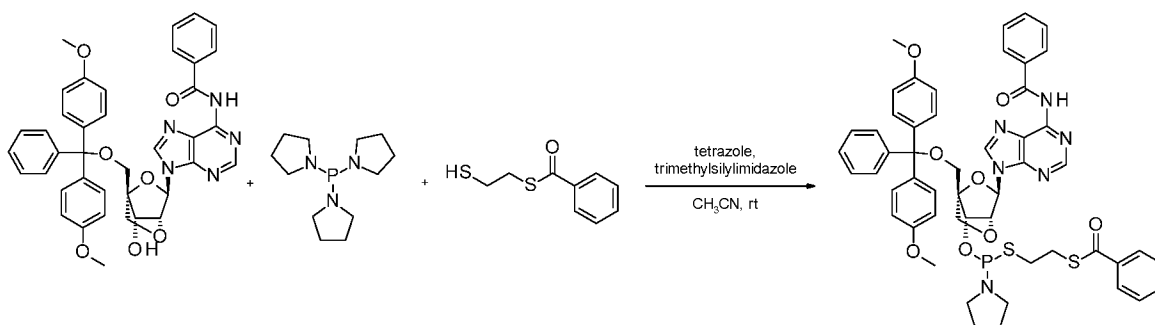


- 1-[(1R,4R,6R,7S)-4-[[bis(4-methoxyphenyl)-phenyl-methoxy]methyl]-7-hydroxy-2,5-dioxabicyclo[2.2.1]heptan-6-yl]-5-methyl-pyrimidine-2,4-dione (2.29 g, 4.00 mmol, 1.0 eq) was dissolved in 60 mL of anhydrous dichloromethane to which a spatula of 3 Å molecular sieves was added. Tripyrrolidin-1-ylphosphane (960 mg, 3.98 mmol, 0.99 eq) was added via syringe followed by seven 0.1 mmol aliquots of tetrazole (7 * 0.4 mL of a 0.5 M solution in anhydrous acetonitrile stored over 3 Å molecular sieves) at 2 min intervals. N-trimethylsilylimidazole (56.0 mg, 0.400 mmol, 0.1 eq) was then added to the reaction. After 5 min, tetrazole (21.6 mL of a 0.5 M solution in anhydrous acetonitrile) was added, immediately followed by the addition of S-(2-sulfanylethyl) benzenecarbothioate (1.04 g, 5.24 mmol, 1.31 eq). The reaction was allowed to proceed for 120 sec. Four identical batches of the reaction were united and quenched by
- 20
- 25

pouring the solution into 600 mL of dichloromethane containing 40 mL of triethylamine. The mixture was immediately washed with saturated sodium bicarbonate (800 mL) followed by 10% sodium carbonate (2 * 800 mL) and brine (800 mL). The organic layer was dried over Na₂SO₄. After 10-15 min the drying agent was removed by filtration.

- 5 Triethylamine (40 mL) was added to the solution which was concentrated using a rotary evaporator to a syrup. The syrup was dissolved in toluene (200 mL) and triethylamine (40 mL), and this solution was pipetted into 4500 mL of vigorously stirred heptane to precipitate the fluffy white product. After most of the heptane was decanted, the white precipitate was collected by filtration through a medium sintered glass funnel and
- 10 subsequently dried under vacuum to give a white solid. The solid was purified by prep-HPLC (Phenomenex Gemini C18, 250x50mm, 10 mm column, 0.05% ammonium hydroxide in water / CH₃CN), and freeze-dried to afford 4.58 g of target compound as a white solid. ³¹P NMR (162 MHz, CD₃CN) δ 167.6, 164.2. ¹H NMR (400 MHz, CD₃CN) δ
- 15 9.16 (br s, 1H), 7.93 (t, *J*=7.41 Hz, 2H), 7.60-7.71 (m, 1H), 7.45-7.57 (m, 4H), 7.24-7.45 (m, 7H), 6.90 (d, *J*=8.93 Hz, 4H), 5.53-5.63 (m, 1H), 4.41-4.64 (m, 2H), 3.74-3.88 (m, 8H), 3.39-3.63 (m, 2H), 3.03-3.32 (m, 5H), 2.77-2.94 (m, 2H), 1.66-1.84 (m, 4H), 1.54-1.66 (m, 3H).

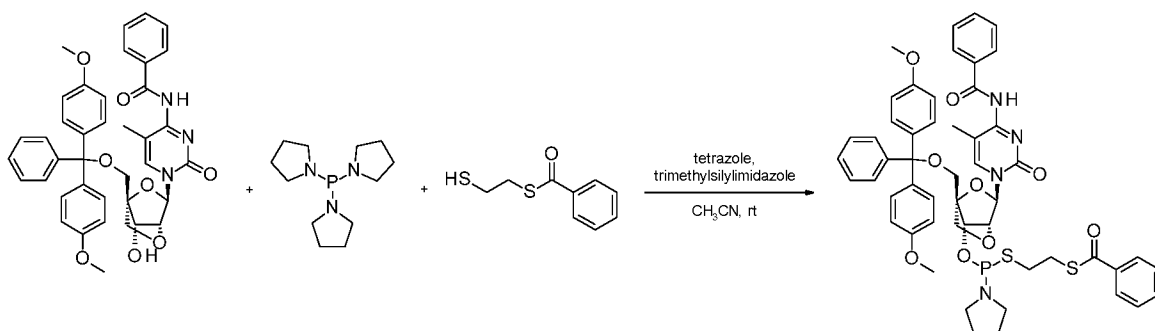
- 1.3: S-[2-[[[(1R,3R,4R,7S)-3-(6-benzamidopurin-9-yl)-1-[[bis(4-methoxyphenyl)-phenyl-methoxy]methyl]-2,5-dioxabicyclo[2.2.1]heptan-7-yl]oxy-pyrrolidin-1-yl-phosphanyl]sulfanylethyl] benzenecarbothioate**
- 20



- N-[9-[(1R,4R,6R,7S)-4-[[bis(4-methoxyphenyl)-phenyl-methoxy]methyl]-7-hydroxy-2,5-dioxabicyclo[2.2.1]heptan-6-yl]purin-6-yl]benzamide (2.74g, 4.00 mmol, 1.0 eq) was dissolved in 60 mL of anhydrous dichloromethane to which a spatula of 3 Å molecular
- 25 sieves was added. Tripyrrolidin-1-ylphosphane (960 mg, 3.98 mmol, 0.99 eq) was added via syringe followed by seven 0.1 mmol aliquots of tetrazole (7 * 0.4 mL of a 0.5 M solution in anhydrous acetonitrile stored over 3 Å molecular sieves) at 2 min intervals. 1-(trimethylsilyl)-1H-imidazole (56.0 mg, 0.400 mmol, 0.1 eq) was then added to the reaction. After 5 min, tetrazole (21.6 mL of a 0.5 M solution in anhydrous acetonitrile)
- 30 was added, immediately followed by the addition of S-(2-sulfanylethyl) benzenecarbothioate (1.04 g, 5.24 mmol, 1.31 eq). The reaction was allowed to proceed for 120 s.

Four identical batches of the reaction were united and quenched by pouring the solution into 600 mL of dichloromethane containing 40 mL of triethylamine. The mixture was immediately washed with saturated sodium bicarbonate (800 mL) followed by 10% sodium carbonate (2 * 800 mL) and brine (800 mL). The organic layer was dried over Na₂SO₄. After 10-15 min the drying agent was removed by filtration. Triethylamine (10 mL) was added to the solution which was concentrated using a rotary evaporator to a syrup. The syrup was dissolved in toluene (100 mL) and triethylamine (20 mL), and this solution was pipetted into 4500 mL of vigorously stirred heptane to precipitate the fluffy white product. After most of the heptane was decanted, the white precipitate was collected by filtration through a medium sintered glass funnel and subsequently dried under vacuum to give a white solid. The solid was purified by prep-HPLC (Phenomenex Gemini C18, 250x50mm, 10 mm column, 0.05% ammonium hydroxide in water / CH₃CN), and freeze-dried to afford 5.26 g of target compound as a white solid. ³¹P NMR (162 MHz, CD₃CN) δ 165.6, 164.7. ¹H NMR (400 MHz, CD₃CN) δ 8.56 (d, *J*=10.76 Hz, 1H), 8.24 (d, *J*=10.27 Hz, 1H), 7.82-7.93 (m, 2H), 7.71-7.80 (m, 2H), 6.92-7.54 (m, 14H), 6.68-6.83 (m, 4H), 6.03 (d, *J*=6.48 Hz, 1H), 4.70-4.90 (m, 2H), 3.81-3.98 (m, 2H), 3.59-3.68 (m, 7H), 3.25-3.47 (m, 2H), 2.81-3.02 (m, 6H), 2.56-2.81 (m, 2H), 1.44-1.72 (m, 4H).

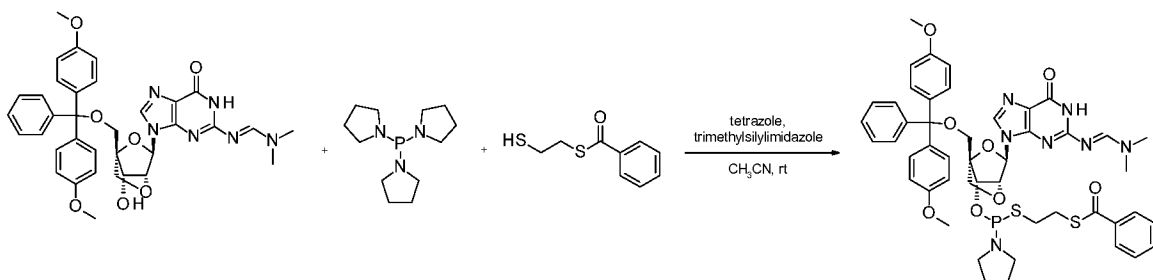
1.4: S-[2-[[[(1R,3R,4R,7S)-3-(4-benzamido-5-methyl-2-oxo-pyrimidin-1-yl)-1-[[bis(4-methoxyphenyl)-phenyl-methoxy]methyl]-2,5-dioxabicyclo[2.2.1]heptan-7-yl]oxy-pyrrolidin-1-yl-phosphanyl]sulfanylethyl] benzenecarbothioate



N-[1-[(1R,4R,6R,7S)-4-[[bis(4-methoxyphenyl)-phenyl-methoxy]methyl]-7-hydroxy-2,5-dioxabicyclo[2.2.1]heptan-6-yl]-5-methyl-2-oxo-pyrimidin-4-yl]benzamide (2.70 g, 4.00 mmol, 1.0 eq) was dissolved in 60 mL of anhydrous dichloromethane to which a spatula of 3 Å molecular sieves was added. Tripyrrolidin-1-ylphosphane (965 mg, 4.00 mmol, 1.0 eq) was added via syringe followed by seven 0.1 mmol aliquots of tetrazole (7 * 0.4 mL of a 0.5 M solution in anhydrous acetonitrile stored over 3 Å molecular sieves) at 2 min intervals. 1-(trimethylsilyl)-1H-imidazole (56.0 mg, 0.400 mmol, 0.1 eq) was then added to the reaction. After 5 min, tetrazole (21.6 mL of a 0.5 M solution in anhydrous acetonitrile) was added, immediately followed by the addition of S-(2-sulfanylethyl) benzenecarbothioate (1.04 g, 5.24 mmol, 1.31 eq). The reaction was allowed to proceed for 120 sec. Four identical batches of the reaction were quenched and united by pouring

the solution into 600 mL of dichloromethane containing 40 mL of triethylamine. The mixture was immediately washed with saturated sodium bicarbonate (800 mL) followed by 10% sodium carbonate (2 * 800 mL) and brine (800 mL). The organic layer was dried over Na₂SO₄. After 10-15 min the drying agent was removed by filtration. Triethylamine (40 mL) was added to the solution which was concentrated using a rotary evaporator to a syrup. The syrup was dissolved in toluene (100 mL) and triethylamine (30 mL), and this solution was pipetted into 4500 mL of vigorously stirred heptane to precipitate the fluffy white product. After most of the heptane was decanted, the white precipitate was collected by filtration through a medium sintered glass funnel and subsequently dried under vacuum to give a white solid. The solid was purified by prep-HPLC (Phenomenex Gemini C18, 250x50mm, 10 mm column, 0.05% ammonium hydroxide in water / CH₃CN) and freeze-dried to afford 2.05 g of target compound as a white solid. ³¹P NMR (162 MHz, CD₃CN) δ 171.2, 167.4. ¹H NMR (400 MHz, CD₃CN) δ 8.18-8.32 (m, 2H), 7.81-7.93 (m, 3H), 7.35-7.60 (m, 14H), 7.17-7.35 (m, 2H), 6.93 (d, *J*=8.93 Hz, 4H), 5.65 (d, *J*=15.04 Hz, 1H), 4.56-4.72 (m, 2H), 3.69-3.90 (m, 8H), 3.45-3.61 (m, 2H), 3.03-3.26 (m, 6H), 2.76-3.02 (m, 2H), 1.65-1.93 (m, 7H).

1.5: S-[2-[[[(1R,3R,4R,7S)-1-[[bis(4-methoxyphenyl)-phenyl-methoxy]methyl]-3-[2-[(E)-dimethylaminomethyleneamino]-6-oxo-1H-purin-9-yl]-2,5-dioxabicyclo[2.2.1]heptan-7-yl]oxy-pyrrolidin-1-yl-phosphanyl]sulfanylethyl] benzenecarbothioate



N'-[9-[(1R,4R,6R,7S)-4-[[bis(4-methoxyphenyl)-phenyl-methoxy]methyl]-7-hydroxy-2,5-dioxabicyclo[2.2.1]heptan-6-yl]-6-oxo-1H-purin-2-yl]-N,N-dimethyl-formamidinium (2.62 mg, 4.00 mmol, 1.0 eq) was dissolved in 200 mL of anhydrous dichloromethane to which a spatula of 3 Å molecular sieves was added. Tripyrrolidin-1-ylphosphane (965 mg, 4.00 mmol, 1.0 eq) was added via syringe followed by seven 0.1 mmol aliquots of tetrazole (7 * 0.4 mL of a 0.5 M solution in anhydrous acetonitrile stored over 3 Å molecular sieves) at 2 min intervals. 1-(trimethylsilyl)-1H-imidazole (56.0 mg, 0.400 mmol, 0.1 eq) was then added to the reaction. After 5 min, tetrazole (21.6 mL of a 0.5 M solution in anhydrous acetonitrile) was added, immediately followed by the addition of S-(2-sulfanylethyl) benzenecarbothioate (1.04 g, 5.24 mmol, 1.31 eq). The reaction was allowed to proceed for 180 s.

Four identical batches were combined and quenched by pouring the solutions into 600 mL of dichloromethane containing 40 mL of triethylamine. The mixture was immediately washed with saturated sodium bicarbonate (800 mL) followed by 10% sodium carbonate (2 * 800 mL) and brine (800 mL). The organic layer was dried over Na₂SO₄. After 10-15 min the drying agent was removed by filtration. Triethylamine (40 mL) was added to the solution which was concentrated using a rotary evaporator to a syrup. The syrup was dissolved in toluene (100 mL) and triethylamine (30 mL), and this solution was pipetted into 4500 mL of vigorously stirred heptane to precipitate the fluffy white product. After most of the heptane was decanted, the white precipitate was collected by filtration through a medium sintered glass funnel and subsequently dried under vacuum to give a white solid. The solid was purified by prep-HPLC (Phenomenex Gemini C18, 250x50mm, 10 mm column, 0.05% ammonium hydroxide in water / CH₃CN) and freeze-dried to afford 3.82 g of target compound as a yellow solid. ³¹P NMR (162 MHz, CD₃CN) δ 167.1, 162.2. ¹H NMR (400 MHz, CD₃CN) δ 9.36 (br s, 1H), 8.63 (d, *J*=16.51 Hz, 1H), 7.78-8.00 (m, 3H), 7.66 (t, *J*=7.62 Hz, 1H), 7.42-7.57 (m, 4H), 7.24-7.40 (m, 7H), 6.89 (d, *J*=8.68 Hz, 4H), 5.92-5.98 (m, 1H), 4.72-4.97 (m, 2H), 3.86-4.05 (m, 2H), 3.78 (2s, 6H), 3.27-3.70 (m, 3H), 2.87-3.20 (m, 12H), 2.67-2.82 (m, 2H), 1.54-1.79 (m, 4H).

Example 2: Oligonucleotide synthesis

Oligonucleotides were synthesized using a MerMade 12 automated DNA synthesizer by Bioautomation. Syntheses were conducted on a 1 μmol scale using a controlled pore glass support (500Å) bearing a universal linker.

In standard cycle procedures for the coupling of DNA and LNA phosphoramidites DMT deprotection was performed with 3% (w/v) trichloroacetic acid in CH₂Cl₂ in three applications of 200 μL for 30 sec. The respective phosphoramidites were coupled three times with 100 μL of 0.1 M solutions in acetonitrile (or acetonitrile/CH₂Cl₂ 1:1 for the LNA-^{Me}C building block) and 110 μL of a 0.1 M solution of 5-(3,5-bis(trifluoromethylphenyl))-1H-tetrazole in acetonitrile as an activator and a coupling time of 180 sec. For thiooxidation a 0.1m solution of 3-amino-1,2,4-dithiazole-5-thione in acetonitrile/pyridine 1:1 was used (3x190 μL, 55 sec). Capping was performed using THF/lutidine/Ac₂O 8:1:1 (CapA, 75 μmol) and THF/*N*-methylimidazole 8:2 (CapB, 75 μmol) for 55 sec.

Synthesis cycles for the introduction of thiophosphoramidites included DMT deprotection using 3% (w/v) trichloroacetic acid in in CH₂Cl₂ in three applications of 200 μL for 30 sec. Commercially available DNA thiophosphoramidites or freshly prepared LNA thiophosphoramidites were coupled three times with 100 μL of 0.15 M solutions in 10% (v/v) CH₂Cl₂ in acetonitrile and 110 μL of a 0.1 M solution of 5-(3,5-bis(trifluoromethylphenyl))-1H-tetrazole in acetonitrile as an activator and a coupling time

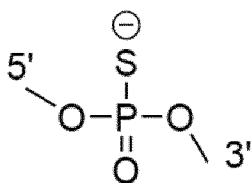
of 600 sec each. Thiooxidation was performed using a 0.1 M solution of 3-amino-1,2,4-dithiazole-5-thione in acetonitrile/pyridine in three applications for 55 sec. Capping was performed using THF/lutidine/Ac₂O 8:1:1 (CapA, 75 μmol) and THF/*N*-methylimidazole 8:2 (CapB, 75 μmol) for 55 sec.

- 5 Upon completion of the automated synthesis, removal of the nucleobase protecting groups and cleavage from the solid support is carried out using an ammonia (32%):ethanol (3:1, v:v) mixture containing 20 mM DTT at 55°C for 15-16 h.

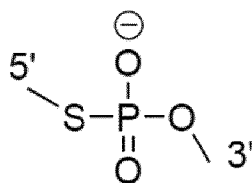
Crude DMT-on oligonucleotides were purified either using a solid phase extraction cartridge and repurification with ion exchange chromatography or by RP-HPLC

- 10 purification using a C18 column followed by DMT removal with 80% aqueous acetic acid and ethanol precipitation.

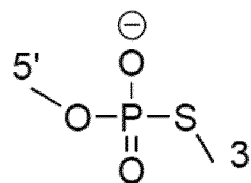
In the following examples we have used the following thio linkage chemistries



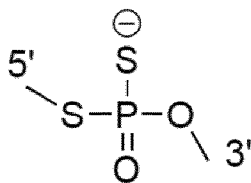
Phosphorothiate



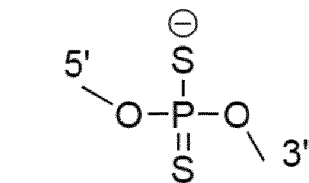
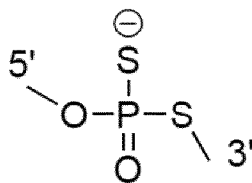
5'S phosphoromonothiate



3'S phosphoromonothiate



Chiral phosphorodithioates



achiral phosphorodithioates

- In the following examples, unless otherwise indicated, the achiral phosphorodithioate linkages (also referred to as P2S) are non-bridging dithioates (as illustrated in formula (IA) or (IB)), and are labelled as *. The compounds used in the example include compounds with the following sequence of nucleobases:
- 15

SEQ ID NO 1: GCATTGGTATTCA

SEQ ID NO 2: TCTCCCAGCGTGCGCCAT

- 20 SEQ ID NO 3: GAGTTACTTGCCAACT

SEQ ID NO 4: TATTTACCTGGTTGTT

SEQ ID NO 5: CAATCAGTCCTAG

The following molecules have been prepared following the above procedure.

Compound ID No.	Compound (SEQ ID NO)	Calculated mass	Found mass
#1	G ^m Ca*ttggtatT ^m CA	4341.6	4341.6
#2	G ^m Cat*tggtatT ^m CA	4341.6	4341.6
#3	G ^m Catt*ggatT ^m CA	4341.6	4341.6
#4	G ^m Cattg*gtatT ^m CA	4341.6	4341.6
#5	G ^m Cattgg*tatT ^m CA	4341.6	4341.6
#6	G ^m Cattggt*atT ^m CA	4341.6	4341.6
#7	G ^m Cattggta*tT ^m CA	4341.6	4341.6
#8	G ^m Cattggtat*T ^m CA	4341.6	4341.6
#9	G ^m Cat*t*ggatT ^m CA	4357.6	4356.8
#10	G ^m Cattggt*at*T ^m CA	4357.6	4356.8
#11	G ^m Cat*tggt*atT ^m CA	4357.6	4357.2
#12	G ^m Catt*ggat*T ^m CA	4357.6	4356.8
#13	G ^m Cat*tggtat*T ^m CA	4357.6	4356.9
#14	G ^m Cat*t*ggat*T ^m CA	4373.7	4373.5
#15	G ^m Catt*ggat*at*T ^m CA	4373.7	4373.1
#16	G ^m Cat*t*ggat*atT ^m CA	4373.7	4373.0
#17	G ^m Cat*t*ggat*at*T ^m CA	4389.8	4389.1
#18	G ^m Ca*ttg*gta*tT ^m CA	4373.7	4373.0
#19	G ^m Ca*tt*gg*ta*tT ^m CA	4389.8	4389.0

#20	G ^m Ca*ttgga*tT ^m CA	4357.6	4356.9
#21	G ^m Ca*ttggtat*T ^m CA	4357.6	4357.1
#22	G ^m Cat*ttgga*tT ^m CA	4357.6	4356.9
#23	G ^m Cattg*gt*atT ^m CA	4357.6	4357.6
#24	G ^m Cattg*g*t*atT ^m CA	4373.7	4373.7
#25	G ^m Cattg*g*t*at*T ^m CA	4389.8	4389.8
#26	G ^m Cattg*g*t*a*t*T ^m CA	4405.8	4405.8
#27	G ^m CattggtatT ^m C*A	4341.6	4342.0
#28	G ^m CattggtatT ^m CA	4341.6	4342.5
#29	G ^m CattggtatT ^m C*A	4357.6	4359.0
#30	G ^m CattggtatT ^m C*A	4373.7	4368.5
#31	G ^m C*attggtatT ^m C*A	4373.7	4369.2
#32	G ^m C*attggtatT ^m C*A	4389.8	4390.6

* Dithioate modification between adjacent nucleotides

A, G, ^mC, T represent LNA nucleotides

a, g, c, t represent DNA nucleotides

all other linkages were prepared as phosphorothioates

5 Example 3: In vitro efficacy and cellular uptake experiments

Primary rat Hepatocytes were plated in 96-well plates and treated in Williams Medium E containing 10% FCS without antibiotics. Cells were treated with LNA solutions in the indicated concentrations in full cell culture medium. After an incubation time of 24 and 72 hrs, respectively, the cells were washed 3 times with PBS containing Ca²⁺ and Mg²⁺ and lysed with 165 uL PureLink Pro lysis buffer. Total RNA was isolated using the PureLink PRO 96 RNA Kit from Thermo Fisher according to the manufacturers instructions and RT-qPCR was performed using the LightCycler Multiplex RNA Virus Master (Roche) with Primer Probe Sets for RnApoB (Invitrogen). The obtained data was normalized to Ribogreen.

Intracellular concentrations of the LNA oligonucleotides were determined using an hybridization based ELISA assay for a variety of compounds. All data points were performed in triplicates and data is given as the average thereof.

The results are shown in Figures 1 to 4.

5 Example 4: Thermal melting (T_m) of oligonucleotides containing a phosphorodithioate internucleoside linkage hybridized to RNA and DNA

The following oligonucleotides have been prepared. Phosphorothioate linkages are designated by the S subscript; Phosphorodithioate linkages according to the invention are designated by the PS2 subscript.

Compound	
1	5'-G _S ^m C _S as ts ts gs gs ts as ts T _S ^m C _{PS2} A -3'
2	5'-G _{PS2} ^m C _S as ts ts gs gs ts as ts T _S ^m C _S A -3'
3	5'-G _{PS2} ^m C _S as ts ts gs gs ts as ts T _S ^m C _{PS2} A -3'
4	5'-G _{PS2} ^m C _S as ts ts gs gs ts as ts T _{PS2} ^m C _{PS2} A -3'
5	5'-G _{PS2} ^m C _{PS2} as ts ts gs gs ts as ts T _S ^m C _{PS2} A -3'
6	5'-G _{PS2} ^m C _{PS2} as ts ts gs gs ts as ts T _{PS2} ^m C _{PS2} A -3'
Control	5'-G _S ^m C _S as ts ts gs gs ts as ts T _S ^m C _S A -3'
DNA Control	5'-ts cs ts cs cs cs as gs cs gs ts gs cs gs cs cs as t -3'
SEQ ID NO 2	

10 Compounds 1 – 6 have the sequence motif SEQ ID NO 1.

The thermal melting (T_m) of compounds **1-6** hybridized to RNA and DNA was measured according to the following procedure.

15 A solution of equimolar amount of RNA or DNA and LNA oligonucleotide (1.5 μM) in buffer (100 mM NaCl, 0.1 mM EDTA, 10 mM Na₂HPO₄, pH 7) was heated to 90 °C for 1 min and then allowed to cool to room temperature. The UV absorbance at 260 nm was recorded using a Cary Series UV-Vis spectrophotometer (heating rate 1 °C per minute; reading rate one per min). The absorbance was plotted against temperature and the T_m values were calculated by taking the first derivative of each curve.

The results are summarized in the Table below and in Figure 5.

RNA				DNA		
	Td	Ta	ΔT_m	Td	Ta	ΔT_m
Control	59,1	57,7	1,5	50,1	47,7	2,4
1	58,0	54,8	3,2	50,0	46,9	3,1
2	58,1	55,7	2,5	49,1	46,7	2,4
3	58,3	55,5	2,8	50,2	47,6	2,6
4	57,5	54,4	3,1	48,4	46,5	1,8
5	57,6	56,3	1,3	48,5	47,4	1,1
6	58,0	55,8	2,2	50,0	46,9	3,1

Td: Temperature of dissociation (denaturation); Ta: Temperature of association (renaturation)

The compounds according to the invention retain the high affinity for RNA and DNA of
5 the control.

Example 5: Serum stability of oligonucleotides containing a phosphorodithioate internucleoside linkage

Stability of oligonucleotides **1-6** in serum from male Sprague-Dawling rats was measured according to the following procedure.

- 10 A 25 μ M oligonucleotide solution in rat serum mixed with Nuclease buffer (30 mM sodium acetate, 1mM zinc sulfate, 300 mM NaCl, pH 4,6) 3:1 were incubated at 37 °C for 0, 5, 25, 52 or 74 hours. Samples 2 μ L were injected for UPLC-MS analysis on a Water Acquity UPLC equipped with a Water Acquity BEH C₁₈, 1,7 μ m column. The analogue peak areas measured at 260 nm compensated with the extinction constants of the different
15 degradation lengths were used to establish the % of uncleaved oligonucleotide.

UPLC eluents: A: 2,5% MeOH, 0,2 M HEP, 16,3 mM TEA B: 60% MeOH, 0,2 M HEP, 16,3 mM TEA

TIME MIN.	FLOW ML/	% A BUFFER	% B BUFFER
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	MIN		
0	0.5	90	10
0.5	0.5	90	10
5	0.5	70	30
6	0.5	70	30
7	0.5	0	100
8	0.5	0	100
9	0.5	90	10
14.9	0.5	90	10
15	0.5	90	10

The results are summarized in Figure 6.

The compounds having at least one phosphorodithioate internucleoside linkage according to the invention have a superior nuclease resistance than the compounds having only
5 phosphorothioate internucleoside linkages.

The initial oligonucleotide degradation seen after 5 hours in compounds **1-6** was found to be caused by the presence of a monothioate impurity.

Example 7: Dithioate Modified Gapmers: Exploring the dithioates in the gap region of LNA gapmers.

10 Compounds Tested

<i>single modification in the gap</i>			
#1	GCa*ttggtatTCA	#5	GCattgg*tatTCA
#2	GCat*tggtatTCA	#6	GCattggt*atTCA

#3	GCatt*ggatTCA	#7	GCattggtat*tTCA
#4	GCattg*gtatTCA	#8	GCattggtat*TCA
<i>cumulation in gap region</i>			<i>dithioate in LNA flanks</i>
#9	GCattg*gt*atTCA	#13	GC*attggtatTCA
#10	GCattg*g*t*atTCA	#14	GCattggtatT*CA
#11	GCattg*g*t*at*TCA	#15	GCattggtatTC*A
#12	GCattg*g*t*a*t*TCA	#16	GC*attggtatT*C*A
Ref.	GCattggtatTCA		
Compounds #1 - #16 and Ref. have the sequence motif shown in SEQ ID NO 1. Upper case letter: beta-D-oxy LNA nucleoside; lower case letter DNA nucleoside; * = achiral phosphorodithioate modified linkages; all other linkages phosphorothioate			

Experimental: The above compounds targeting ApoB mRNA, were tested in primary rat hepatocytes using gymnotic uptake, with incubation for 72 hrs with a compound concentration of 2 μ M. The target mRNA levels were then measured using RT-PCR.

5 Results are shown in Figure 7.

The results shown in figure 7 illustrate that both single and multiple achiral phosphorodithioates are accommodated in the gap and flank regions. The use of more than 3 or 4 achiral phosphorodithioates in the gap may tend to reduce potency as compared to the use of multiple achiral phosphorodithioates in the flank region.

10 Example 8: Positional dependency on activity – design optimisation

Compounds Tested

<i>2 modifications</i>			
#1	GCat*t*gggtatTCA	#6	GCat*tggtat*TCA
#2	GCattgggt*at*TCA	#7	GCa*ttggta*tTCA
#3	GCat*tggt*atTCA	#8	GCa*ttggat*TCA
#4	GCatt*gggt*atTCA	#9	GCat*tggtat*tTCA
#5	GCatt*gggtat*TCA		
<i>3 modifications</i>			<i>4 modifications</i>
#10	GCat*tggt*at*TCA	#15	GCat*t*gggt*at*TCA
#11	GCat*t*gggtat*TCA	#16	GCa*tt*gg*ta*tTCA
#12	GCatt*ggta*t*TCA		
#13	GCat*t*gggt*atTCA		
#14	GCa*ttg*gta*tTCA		
Ref.	GCattgggtatTCA		
Compounds #1 - #16 and Ref. have the sequence motif shown in SEQ ID NO 1. Upper case letter: beta-D-oxy LNA nucleoside; lower case letter DNA nucleoside; * = achiral phosphorodithioate modified linkages; all other linkages phosphorothioate			

Experimental: The above compounds targeting ApoB mRNA, were tested in primary rat hepatocytes using gymnotic uptake, with incubation for 72 hrs with a compound

concentration of 2 μ M. The target mRNA levels were then measured using RT-PCR. Results are shown in Figure 8.

Example 9: Cellular Uptake of achiral phosphorodithioate gapmers

Compounds Tested

<i>single modification in the gap</i>			
#1	GCa*ttggtatTCA	#5	GCattgg*tatTCA
#2	GCat*tggtatTCA	#6	GCattggt*atTCA
#3	GCatt*ggtatTCA	#7	GCattggtat*tTCA
#4	GCattg*gtatTCA	#8	GCattggtat*tTCA
Ref.	GCattggtatTCA		

- 5 Compounds #1 - #16 and Ref. have the sequence motif shown in SEQ ID NO 1.

Upper case letter: beta-D-oxy LNA nucleoside; lower case letter DNA nucleoside;

* = achiral phosphorodithioate modified linkages; all other linkages phosphorothioate

- Experimental:** The above compounds targeting ApoB mRNA, were tested in primary rat hepatocytes using gymnotic uptake, with incubation for 72 hrs with a compound concentration of 2 μ M. Oligonucleotide content was determined using a hybridization based ELISA assay. The results are shown in Figures 9A and 9B.
- 10

Without exception, the inclusion of an achiral phosphorodithioate provided enhanced cellular uptake. There was however a diversity in the uptake improvement depending upon the position of the achiral phosphorodithioate linkage.

- 15 **Example 10:** Increasing the achiral phosphorodithioate load in the flank region of a gapmer

Compounds Tested (Sequence motif = SEQ ID NO 1)

modifications in the flanks

		IC50 [nM]			IC50 [nM]
●	GCattggtatTC*A	7.3	▼	G*CattggtatT*C*A	9.2
■	G*CattggtatTCA	10.4	◆	G*C*attggtatTC*A	8.9
▲	G*CattggtatTC*A	6.8	○	G*C*attggtatT*C*A	4.9
Ref.	GCattggtatTCA	33.3			

Upper case letter: beta-D-oxy LNA nucleoside; lower case letter DNA nucleoside;

* = achiral phosphorodithioate modified linkages; all other linkages phosphorothioate

- Experimental:** The above compounds targeting ApoB mRNA, were tested in primary rat hepatocytes using gymnotic uptake, with incubation for 72 hrs with a compound concentration of 2μM. The target mRNA levels were then measured using RT-PCR. The results are shown in Figures 10A and 10B.

The introduction of achiral phosphorodithioate modifications in the flank regions of gapmers provided without exception a pronounced increase in potency, with a reduction in IC50 of 3 – 7 x. Interestingly, an increase in the number of chiral phosphorodithioate modifications in the flanks results in a lower IC50.

Example 11: Effect of achiral phosphorodithioate linkages in different cell types, in vitro.

Compounds Tested (Sequence motif = SEQ ID NO 3)

<i>modification in the flanks</i>			
#1	GAGttacttgccaAC*T	#5	G*A*GttacttgccaAC*T
#2	G*AGttacttgccaACT	#6	G*A*GttacttgccaA*C*T
#3	G*AGttacttgccaAC*T	#7	G*A*G*ttacttgccaA*C*T
#4	G*AGttacttgccaA*C*T		

Ref.	GAGTtacttgccaACT		
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Upper case letter: beta-D-oxy LNA nucleoside; lower case letter DNA nucleoside;

* = achiral phosphorodithioate modified linkages; all other linkages phosphorothioate

- The above compounds which target Malat-1 were tested in three in vitro cell systems: human primary skeletal muscles, human primary bronchial epithelial cells and mouse fibroblasts (LTK cells) using gymnotic uptake for 72 hours, at a range of concentrations to determine the compound potency (IC₅₀).

Concentration range for LTK cells: 50 μM, 1/2 log dilution, 8 concentrations.

RNA levels of Malat1 were quantified using qPCR (Normalised to GAPDH level) and IC₅₀ values were determined.

- 10 The IC₅₀ results are shown in figure 11. The introduction of achiral phosphorodithioate provided a reliable enhanced potency in skeletal muscle cells, and in general gave an improved potency into mouse fibroblasts. The effect in human bronchial epithelial cells was more compound specific, however in some compounds (#5) were markedly more potent than the reference compound.
- 15 **Example 12:** In vitro rat serum stability of 5' and 3' end protected LNA oligonucleotides.

Compounds Tested (Sequence motif = SEQ ID NO 1)

#1	PS/DNA oligonucleotide
#2	GCattggtatTCA
#3	G*GattggtatTCA
#4	GCattggtatTC*A
#5	G*GattggtatTC*A
#6	G*GattggtatT*C*A

#7	G*C*attggtatTC*A
#8	G*C*attggtatT*C*A

Upper case letter: beta-D-oxy LNA nucleoside; lower case letter DNA nucleoside;

* = achiral phosphorodithioate modified linkages; all other linkages phosphorothioate

Experimental – see example 5.

- The results are shown in figure 12. We have identified that the 3' end of LNA
- 5 phosphorothioate oligonucleotides are more susceptible to serum nucleases than previously thought and this appears to be related to the chirality of the phosphorothioate linkage(s) at the 3' end of the oligonucleotide – as illustrated by the rapid cleavage of 50% of the parent oligonucleotide #1. The 5' end protection with an achiral phosphorodithioate provided an improved protection. The 3' end protection with an achiral phosphorodithioate
- 10 provided complete protection to rat serum exonucleases – the slight reduction seen for compound #4 - #8 was correlated to a monothioate impurity.

The 5' and/or 3' end protection of antisense oligonucleotides with the achiral phosphorothioate linkages is therefore considered to provide a solution to a major instability problem with stereorandom and stereodefined phosphorothioates.

- 15 **Example 13:** In vivo assessment of gapmers with achiral phosphorodithioate linkages in the flanks.

Compounds Tested (Sequence motif = SEQ ID NO 1)

#1	GCattggtatTC*A
#2	G*CattggtatTCA
#3	G*CattggtatTC*A
#4	G*CattggtatT*C*A
#5	G*C*attggtatTC*A
#6	G*C*attggtatT*C*A

#7	G*C* <u>attggtat</u> T*C*A
#8	GCat* <u>tggt</u> *at*TCA
#9	<u>GCat</u> * <u>tggt</u> * <u>at</u> * <u>TCA</u>
Ref.	GCattggtatTCA

Upper case letter: beta-D-oxy LNA nucleoside; lower case letter DNA nucleoside;

* = achiral phosphorodithioate modified linkages; all other linkages phosphorothioate. Note the underlined bold nucleosides are linked at the 3' position by stereodefined phosphorothioate internucleoside linkages. Compound #7 has a stereodefined motif in the gap region of SSRSSRSR (S = Sp, R = Rp). The backbone motif of compound #9 = RRSPRSSPSS, wherein S = Sp, R = Rp, and P = achiral PS2 linkage (*) .

Experimental: The above compounds targeting ApoB were administered to female C57BL/6JBom mice, using a1 mg/kg single iv dose, and were sacrificed on day 7, n=5. The mRNA reduction in the liver was measured using RT-PCR and the results are shown in Figure 13.

The results show that in general the introduction of the achiral phosphorodithioate internucleoside linkages provides an improved potency, notably all the compounds with achiral phosphorodithioate linkages in the flank regions show improved potency. As illustrated in the in vitro experiment, the use of multiple phosphorodithioate linkages in the gap region (#8) was accommodated without a notable loss of potency. Of particular interest is the combined effect of gapmer designs with stereodefined phosphorothioate linkages in the gap region, with achiral phosphorodithioate linkages in the flanks, illustrating a synergy in combining these linkages technologies with an antisense oligonucleotide.

Example 14: In vivo tissue content in liver of gapmers with achiral phosphorodithioates with modified flanks and gap region.

Compounds and experimental – see example 13. The results of the tissue content (determined by hybridisation based ELISA to measure content in liver and kidney samples from the sacrificed animals) is shown in Figure 14A & B. Note that there was an experimental error for compound #1 – see Figure 14B data.

Results: Figure 14A. All the antisense oligonucleotides which contained the achiral phosphorodithioate linkages had a higher tissue uptake/content as compared to the

reference compound. Figure 14B shows that the introduction of the achiral phosphorodithioate linkage enhanced the biodistribution (as determined by the liver/kidney ratio) of all the compounds tested.

Example 15: Metabolite analysis from in vivo experiment

- 5 Compounds and experimental – see example 13. Metabolite analysis was performed using the methods disclosed in C. Husser et al., Anal. Chem. 2017, 89, 6821.

The results are shown in Figures 15A and 15B. The phosphorodithioate modification efficiently prevents 3'-exonucleolytic degradation in vivo. There remains some endonuclease cleavage (note compounds #1 – 6 tested all have DNA phosphorothioate gap regions so this was expected). Given the remarkable exonuclease protection it is considered that the use of achiral phosphorodithioate linkages within antisense oligonucleotides may be used to prevent or limit endonuclease cleavage. The enhanced nuclease resistance of achiral phosphordithioates is expected to provide notable pharmacological benefits, such as enhanced activity and prolonged duration of action, and possibly avoidance of toxic degradation products.

Example 16: In vivo - Long term liver activity (ApoB)

Compounds tested (Sequence motif = SEQ ID NO 1):

Ref.	GCattggtatTCA
#1	G*C*attggtatT*C*A
#2	<u>GCattggtatTCA</u>
#3	G*C* <u>attggtat</u> T*C*A

Upper case letter: beta-D-oxy LNA nucleoside; lower case letter DNA nucleoside;

* = achiral phosphorodithioate modified linkages; all other linkages phosphorothioate. Note the

- 20 underlined bold nucleosides are linked at the 3' position by stereodefined phosphorothioate internucleoside linkages. Compound #3 has a stereodefined motif in the gap region of SSRSSSR (S = Sp, R = Rp). The backbone motif of compound #2 = RRSSRRSS, wherein S = Sp, R = Rp, and P = achiral PS2 linkage (*).

Experimental: As in example 13, however sacrifice was performed at day 7 or 21.

- 25 The results are shown in Figure 16. Compared to the phosphorothioate reference compound, the introduction of the achiral phosphorodithioate provided a prolonged

- duration of action in the liver and this was correlated with a higher tissue content at 21 days. Notably, the combination of phosphorodithioate linked flank regions with stereodefined phosphorothioate linkages in the gap region provided further benefit with regards to prolonged potency and duration of action, again emphasising the remarkable synergy in combining achiral phosphorodithioate internucleoside linkages with stereodefined phosphorothioate linkages in antisense oligonucleotides.

Example 17: In vivo study using Malat-1 targeting achiral phosphorodithioates modified gapmers.

Compounds Tested (Sequence motif = SEQ ID NO 3)

Ref.	GAGttacttgccaACT
Increasing P2S load in flanks	
#1	G*AGttacttgccaACT
#2	GAGttacttgccaAC*T
#3	G*AGttacttgccaAC*T
#4	G*AGttacttgccaA*C*T
#5	G*A*GttacttgccaAC*T
#6	G*A*GttacttgccaA*C*T
#7	G*A*G*ttacttgccaA*C*T

- 10 Upper case letter: beta-D-oxy LNA nucleoside; lower case letter DNA nucleoside;
* = achiral phosphorodithioate modified linkages; all other linkages phosphorothioate.

Experimental:

In vitro: Mouse LTK cells were used to determined the in vitro concentration dose response curve – measuring the MALAT-1 mRNA inhibition.

- 15 **In vivo:** Mice (C57/BL6) were administered 15mg/kg dose subcutaneously of the oligonucleotide in three doses on day 1, 2 and 3 (n=5). The mice were sacrificed on day 8,

and MALAT-1 RNA reduction and tissue content was measured for liver, heart, kidney, spleen and lung. The parent compounds was administered in two doses 3*15mg/kg and 3*30mg/kg.

Results: The in vitro results are shown in Figure 17 – compounds with 1, 2, 3 and 4
 5 achiral phosphorodithioates in the flanks were found to be highly potent in vitro. The compound #7 with 5 achiral phosphorodithioates in the flanks was found to have a lower potency than those with 1 – 4 achiral phosphorodithioates in the flanks. The most potent compounds #1, #2 and #6 were selected for the in vivo study. The in vivo results are shown in Figure 17B (heart) – which illustrates that the achiral phosphorodithioate
 10 compounds were about twice as potent in knocking down MALAT-1 in the heart as the reference compound. Notably the use of the achiral phosphorodithioate internucleoside linkage between the two 3' terminal nucleosides of the antisense oligonucleotides provided a marked improvement over the equivalent 5' end protected oligonucleotide.

Figure 17C shows the results of the tissue content analysis from the in vivo study. All
 15 three oligonucleotide containing the achiral phosphorodithioate internucleoside linkages had higher tissue content in liver. The di-thioates results in similar or higher content in heart and liver, and lower content in kidney, again illustrating superiority over PS-modified antisense oligonucleotides. Notably the tissue content in heart was only higher for compound 1, indicating that the enhanced in vivo potency may not be a consequence of
 20 the tissue content, but a higher specific activity.

Example 18: Achiral monophosphothioate modifications tested do not provide the portable benefits seen with achiral phosphorodithioate linkages.

Compounds Tested (Sequence motif = SEQ ID NO 1)

#1	GCa [■] ttggtatTCA	#9	GC [†] attggtatTCA
#2	GCat [■] tggtatTCA	#10	GCa [†] ttggtatTCA
#3	GCatt [■] ggtatTCA	#11	GCat [†] tggtatTCA
#4	GCattg [■] gtatTCA	#12	GCatt [†] ggtatTCA
#5	GCattgg [■] tatTCA	#13	GCattg [†] gtatTCA
#6	GCattggt [■] atTCA	#14	GCattgg [†] tatTCA

#7	GCattggta [■] tTCA	#15	GCattggt [†] atTCA
#8	GCattgggat [■] TCA	#16	GCattggta [†] tTCA
Ref.	GCattgggatTCA		

Upper case letter: beta-D-oxy LNA nucleoside; lower case letter DNA nucleoside;

[■] = 3'-S phosphorothioate linkage, all other linkages are phosphorothioate. [†] = 5'-S phosphorothioate linkage, all other linkages are phosphorothioate.

In this study we synthesised a series of 3' or 5' S modified phosphorothioates

- 5 oligonucleotide gapmers targeting ApoB – the positioning of the sulfur in the backbone linkages results in an achiral internucleoside linkage. For synthesis methods see WO2018/019799.

The compounds were tested in vitro as previously described – e.g. see example 8.

- 10 The results are shown in figure 18A: The results show that in general the achiral monophosphorothioates were detrimental to potency of the compounds, although in some instances the compounds retained potency. This appears to correlate with the cellular content (figure 18B).

Example 19: Chiral phosphorodithioate modifications can provide benefits to antisense oligonucleotide gapmers.

- 15 **Compounds Tested** (Sequence motif = SEQ ID NO 1)

#1	GCa [♦] ttggatTCA
#2	GCat [♦] tggtatTCA
#3	GCatt [♦] ggtatTCA
#4	GCattg [♦] gtatTCA
#5	GCattgg [♦] tatTCA
#6	GCattggt [♦] atTCA

#7	GCattggta♦tTCA
#8	GCattggtat♦TCA
Ref.	GCattggtatTCA

Upper case letter: beta-D-oxy LNA nucleoside; lower case letter DNA nucleoside;

♦ = chiral phosphorodithioate linkage, all other linkages are phosphorothioate.

In this study we synthesised a series of stereorandom chiral phosphorodithioates oligonucleotide gapmers targeting ApoB – the positioning of the sulfur in the backbone linkages results in an chiral internucleoside linkage.

The compounds were tested in vitro as previously described – e.g. see example 8.

The results are shown in figure 19A: The results show that in some positions the chiral phosphorodithioate compounds were as potent as the reference compound, indicating the chiral phosphorodithioate was not incompatible with antisense functionality – however the benefit was compound specific (i.e. does not appear portable). A similar picture is seen with regards to cellular uptake (Figure 19B), although there does not appear to be a correlation between antisense activity and cellular uptake.

Example 20: In vivo study using Htra-1 targeting achiral phosphorodithioates modified gapmers.

15 Compounds Tested

All compounds have the sequence: TATttacctggtTGTT (SEQ ID NO 4), wherein capital letters are beta-D-oxy LNA nucleosides, lowercase letters are DNA nucleosides. In the following table, the backbone motif represents the pattern of backbone modifications for each internucleoside linkage starting at the linkage between the 5' dinucleotide, and finishing with the internucleoside linkage between the 3' dinucleotide (left to right). X = stereorandom phosphorothioate internucleoside linkage, P = achiral phosphorodithioate (*), S = Sp stereodefined phosphorothioate internucleoside linkage, R = Rp stereodefined phosphorothioate internucleoside linkage.

Htra1#Parent	TATttacctggtTGTT	XXXXXXXXXXXXXXXXXX
Htra1#1	TATttacctggtTGTT	XXXPXXXXXXXXXXXXX
Htra1#2	TATttacctggtTGTT	XXXXPXXXXXXXXXXXXX

Htra1#3	TATttacctggtTGTT	XXXXXPXXXXXXXXXX
Htra1#4	TATttacctggtTGTT	XXXXXPXXXXXXXXXX
Htra1#5	TATttacctggtTGTT	XXXXXPXXXXXXXXXX
Htra1#6	TATttacctggtTGTT	XXXXXPXXXXXXXXXX
Htra1#7	TATttacctggtTGTT	XXXXXPXXXXXXXXXX
Htra1#8	TATttacctggtTGTT	XXXXXPXXXXXXXXXX
Htra1#9	TATttacctggtTGTT	XXXXXPXXXXXXXXXX
Htra1#10	TATttacctggtTGTT	XXXXPPPPXXXXXXXXX
Htra1#11	TATttacctggtTGTT	XXXXPPPPXXXXXXXXX
Htra1#12	TATttacctggtTGTT	XXXXPPPPXXXXXXXXX
Htra1#13	TATttacctggtTGTT	PSRRRSSRRRRRRP
Htra1#14	TATttacctggtTGTT	PSRRRSSRRRRPXP
Htra1#15	TATttacctggtTGTT	PRRRRSSRRRRRSP
Htra1#16	TATttacctggtTGTT	PRRRRSSRRRRRSS
Htra1#17	TATttacctggtTGTT	RRRRRSSRRRRRSP
Htra1#18	TATttacctggtTGTT	PXPRRSSRRRRPXP
Htra1#19	TATttacctggtTGTT	PXXRRSSRRRRXXP
Htra1#20	TATttacctggtTGTT	PXXXXXXXXXXXXXXXXX
Htra1#21	TATttacctggtTGTT	XXPXXXXXXXXXXXXXXXX
Htra1#22	TATttacctggtTGTT	XXXXXXXXXXXXXXXXPXX
Htra1#23	TATttacctggtTGTT	XXXXXXXXXXXXXXXXXP
Htra1#24	TATttacctggtTGTT	PXXXXXXXXXXXXXXXXXP
Htra1#25	TATttacctggtTGTT	PXPXXXXXXXXXXXPXP

Htra1#26	TATttacctggtTGTT	XXXXXXXXXXXXXXXX
Htra1#27	TATttacctggtTGTT	PPXXXXXXXXXXXXXP
Htra1#28	TATttacctggtTGTT	PXXXXXXXXXXXXXPP
Htra1#29	TATttacctggtTGTT	PPXXXXXXXXXXXXXP
Htra1#30	TATttacctggtTGTT	PPXXXXXXXXXXXXPP
Htra1#31	TATttacctggtTGTT	PPXXXXXXXXXXXXPPP
Htra1#32	TATttacctggtTGTT	PPXXXXXXXXXXXXPP
Htra1#33	TATttacctggtTGTT	PPXXXXXXXXXXXXPPP
Htra1#34	TATttacctggtTGTT	PSPRRSSSSRRRPRP
Htra1#35	TATttacctggtTGTT	PSPRRSSSSRRRPSP
Htra1#36	TATttacctggtTGTT	PRPRSSSSRRRPSP
Htra1#37	TATttacctggtTGTT	PRPRSSSSRRRPRP
Htra1#38	TATttacctggtTGTT	PPPRSSSSRRRPPP

Experimental:

Human glioblastoma U251 cell line was purchased from ECACC and maintained as recommended by the supplier in a humidified incubator at 37°C with 5% CO₂. For assays, 15000 U251 cells/well were seeded in a 96 multi well plate in starvation media (media recommended by the supplier with the exception of 1% FBS instead of 10%). Cells were incubated for 24 hours before addition of oligonucleotides dissolved in PBS. Concentration of oligonucleotides: 5, 1 and 0.2 µM. 4 days after addition of oligonucleotides, the cells were harvested. RNA was extracted using the PureLink Pro 96 RNA Purification kit (Ambion, according to the manufacturer's instructions). cDNA was then synthesized using M-MLT Reverse Transcriptase, random decamers RETROscript, RNase inhibitor (Ambion, according the manufacturer's instruction) with 100mM dNTP set PCR Grade (Invitrogen) and DNase/RNase free Water (Gibco). For gene expressions analysis, qPCR was performed using TagMan Fast Advanced Master Mix (2X) (Ambion) in a duplex set up. Following TaqMan primer assays were used for qPCR: HTRA1, Hs01016151_m1 (FAM-MGB) and house keeping gene, TBP, Hs4326322E (VIC-MGB)

from Life Technologies. EC50 determinations were performed in Graph Pad Prism6. The relative HTRA1 mRNA expression level in the table is shown as % of control (PBS-treated cells).

Results:

	mRNA level remaining at various doses				Potency	Max Efficacy
	5 μ M	1 μ M	0.2 μ M	1 μ M	EC50 [μ M]	mRNA level [% of ctrl]
Htra1#Parent	18	38	116	58	1,16	5,9
Htra1#1	34					
Htra1#2	50					
Htra1#3	28					
Htra1#4	44					
Htra1#5	39					
Htra1#6	47					
Htra1#7	41					
Htra1#8	44					
Htra1#9	47					
Htra1#10	36					
Htra1#11	53					
Htra1#12	36					
Htra1#13	11	57	97			
Htra1#14	3	18	83			

Htra1#15	3	18	85			
Htra1#16	4	24	85			
Htra1#17	3	19	108			
Htra1#18	2	10	76		0,15	4,0
Htra1#19	4	35	90		0,44	3,7
Htra1#20	25	87	96	57		
Htra1#21	22	73	78			
Htra1#22	24		100			
Htra1#23	20	50	117	53	0,91	9,0
Htra1#24	5	51	136	44		
Htra1#25	3	27	69			
Htra1#26	27	72	93			
Htra1#27	7	30	99		0,35	4,7
Htra1#28				67		
Htra1#29				55		
Htra1#30				56		
Htra1#31				54		
Htra1#32				61		
Htra1#33				54		
Htra1#34				54	0,78	5,1
Htra1#35				20	0,17	3,6
Htra1#36				15	0,13	3,1
Htra1#37				42	0,69	3,9

Htra1#38				24	0,23	4,2
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Example 21: A PS2 walk on a LNA Mixmer targeting TNFRSF1B exon 7 skipping

We have previously identified that the skipping of *TNFRSF1B* exon 7 using a mixmer (13'mer) SSO#26 – is highly effective in targeting the 3' splice site of intron 6 - exon 7 of

5 TNFRSF1B (see WO2008131807 & WO2007058894 for background information).

This experiment was established to determine whether the presence of phosphorodithioate linkages of formula (IA) or (IB) (PS2) can be useful in further enhancing the splice modulation activity of splice switching oligonucleotides. To determine the effect, we introduced phosphorodithioates linkages of formula (IA) or (IB) in different positions of

10 the parent oligonucleotide SSO#26 and synthesized the following compounds (Table below).

Compounds tested: Dithioate modified oligonucleotides of the parent oligonucleotide (SSO#26). Phosphorodithioate internucleoside linkages of formula ((IA) or (IB)) were introduced in positions marked with a *, all other internucleoside linkages are

15 phosphorothioate internucleoside linkages (stereorandom), capital letters represent beta-D-oxy LNA nucleosides, and LNA C are 5-methyl-cytosine, lower case letters represent DNA nucleosides.

	Compounds (Sequence motif = SEQ ID NO 5)		Compounds
SSO#1	CAaT*cAG*tcCtA*G	SSO#14	CAaTcAGtcCt*AG
SSO#2	CAaTcAG*tcCtA*G	SSO#15	CAaTcAGtcCtA*G
SSO#3	C*AaTcAGtcC*tAG	SSO#16	C*A*aT*cA*G*tcC*tA*G
SSO#4	C*AaTcAGtcCtAG	SSO#17	C*AaT*cAG*tcC*tA*G
SSO#5	CA*aTcAGtcCtAG	SSO#18	C*A*aTc*A*GtcCt*A*G
SSO#6	CAa*TcAGtcCtAG	SSO#19	C*A*aTcAG*t*cCt*A*G
SSO#7	CAaT*cAGtcCtAG	SSO#20	C*A*a*T*cA*G*t*cCtAG

SSO#8	CAaTc*AGtcCtAG	SSO#21	CAaTcA*G*t*cCt*A*G
SSO#9	CAaTcA*GtcCtAG	SSO#22	CAa*Tc*AGt*c*Ct*AG
SSO#10	CAaTcAG*tCtAG	SSO#23	CAa*Tc*AGt*cCt*AG
SSO#11	CAaTcAGt*cCtAG	SSO#24	CAa*TcAGt*c*Ct*AG
SSO#12	CAaTcAGtc*CtAG	SSO#25	CAa*Tc*AGtc*CtAG
SSO#13	CAaTcAGtcC*tAG	SSO#26	CAaTcAGtcCtAG

Experimental:

Oligonucleotide uptake and exon skipping in Colo 205 cells (human colorectal adenocarcinoma) was analyzed by gymnotic uptake at two different concentrations (5 μ M and 25 μ M). Cells were seeded in 96 well plates (25,000 cells per well) and the oligonucleotide added. Three days after addition of oligonucleotides, total RNA was isolated from 96 well plates using Qiagen setup. The percentage of splice-switching was analyzed by droplet digital PCR (BioRad) with a FAM-labelled probe spanning the exon 6–8 junction (exon 7 skipping) and the total amount of *TNFRSF1B* (wild type and exon 7 skipped) was analyzed with a HEX-labelled probe and primers from IDT spanning exon 2-3. The presence of a phosphorodithioate linkage has an effect on the ability of an oligonucleotide to introduce exon skipping (figure 20). At 5 μ M, the most potent PS2 oligonucleotide increases the exon skipping by more than two fold, where the parent (SSO#26) shows approximately 10% exon skipping, SSO#25 shows more than 20% exon skipping. At 25 μ M, the most potent oligonucleotide reaches more than 60% exon skipping (SSO#7), again more than 2 fold better than the parent. Oligonucleotide SSO#22, in which all DNA nucleotides have a dithioate modification (PS2) instead of the phosphorothioate modification (PS) shows increased activity, compared to the parent, and is the third most potent oligonucleotide at 5 μ M, and second most potent splice switching oligonucleotide at 25 μ M (figure 20). Exchanging all linkages between LNA nucleosides with a PS2 linkage (SSO#16) however reduced the potency in splice switching compared to the parent oligonucleotide (figure 20). Furthermore, it is clear that introducing a PS2 at certain positions, may not be beneficial for the exon skipping activity and at 5 μ M, SSO#1, SSO#9, SSO#11, SSO#12 and SSO#14 do not show significant splice switching activity at the lower concentration, but all were effective at the higher concentration (Figure 20). This examples illustrate that the PS2 linkage is compatible with splice modulating oligonucleotides and further emphasizes a clear benefit in introducing PS2 linkages adjacent to DNA nucleosides, or between adjacent DNA nucleosides, within the mixmer

oligonucleotide, such as LNA mixmers – these designs were notably more effective in modulating splicing.

Materials and methods

Assay to detect *TNFRSF1B* exon 7 skipping by droplet digital PCR

- 5 **Forward sequence:** CAACTCCAGAACCCAGCACT (SEQ ID NO 6)
Reverse sequence: CTTATCGGCAGGCAAGTGAG (SEQ ID NO 7)
Probe Sequence: GCACAAGGGCTTCTCAACTGGAAGAG (SEQ ID NO 8)
Fluorophore: FAM

Assay to detect total amount of *TNFRSF1B*

- 10 IDT assay **Hs.PT.58.40638488 spanning exon 2-3**

Example 22: The stability of mixmer oligos containing phosphorodithioates modifications

- Three dithioate modified oligonucleotides of the parent (**SSO#26**) were selected for stability assay using S1 nuclease (table 2). The selected oligonucleotides were incubated at
- 15 37°C at 25 µM for either 30 min or 2h in 100 µL reaction buffer containing 1x S1 Nuclease buffer, and 10U of S1 nuclease according to manufacturer's instruction (Invitrogen, Catalogue no. 18001-016). The S1 nuclease reaction was stopped by adding 2 µL of 500 mM EDTA solution to the 100 µL reaction mixture. 2.5 µL of the reaction mixture was diluted in Novex™ TBE-Urea 2x sample buffer (LC6876 Invitrogen) and
- 20 loaded onto Novex™ 15% TBE-Urea gels (EC6885BOX, Invitrogen). The gels were run for approximately 1 hour at 180 V, afterwards gel images were acquired with SYBR gold staining (S11494, Invitrogen) and the ChemiDoc™ Touch Imaging System (BIO-RAD).

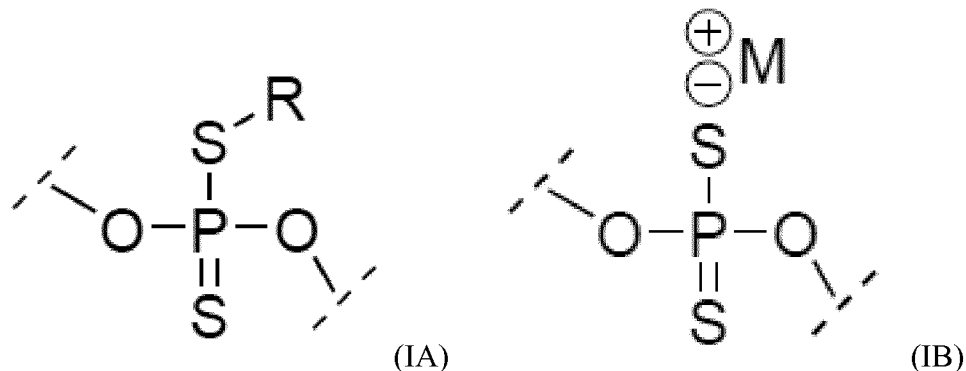
- The stability of the PS2 containing oligonucleotides was tested with 30 and 120 minutes incubation of the S1 nuclease. The position of the PS2 linkage is influencing the stability,
- 25 and the presence of a PS2 3'to a DNA nucleotide (SSO#14) has the greatest impact (figure 21). After 30 minutes of incubation with S1 nuclease, the parent oligonucleotide is almost degraded, whereas the PS2 modified oligos shows a strong band representing the 13'mer. In addition, SSO#14 shows stronger bands representing degradation products indicating a stabilization of the remaining oligo, even after the initial cleavage by S1 nuclease (figure
- 30 21, lane 5+9).

These data illustrate that the presence of a phosphorodithioates when introduced into oligonucleotides, such as mixmer oligonucleotides, provides protection against endonuclease activity – and surprisingly this is achieved whilst maintaining efficacy of

- the oligonucleotides, indeed as shown in the present experiments, the splice modulating activity may be notably improved. It is considered that PS2 linkages adjacent to DNA nucleosides, or between DNA nucleosides, in a mixmer oligonucleotides, herein illustrated by mixmers comprising LNA and DNA nucleosides enhances endonuclease stability. For
- 5 use in antisense oligonucleotides, such as mixmers (SSOs or antimiRs for example), it is therefore considered that using PS2 linkages between contiguous DNA nucleosides is beneficial. Such benefits can also be provided by using a 5' or 3' PS2 linkage adjacent to a DNA nucleoside which is flanked 5' or 3' (respectively) by a 2'sugar modified nucleoside, such as LNA or MOE.
- 10 The invention therefore further provides improved antisense oligonucleotides for use in occupation based mechanisms, such as in splice modulating or for microRNA inhibition.

Claims

1. An oligonucleotide comprising at least one phosphorodithioate internucleoside linkage of formula (IA) or (IB)



- 5 wherein one of the two oxygen atoms is linked to the 3' carbon atom of an adjacent nucleoside (A¹) and the other one is linked to the 5' carbon atom of another adjacent nucleoside (A²), wherein at least one of the two nucleosides (A¹) and (A²) is a LNA nucleoside and wherein in (IA) R is hydrogen or a phosphate protecting group, and in (IB) M⁺ is a cation, such as a metal cation, such as an alkali metal cation, such as a Na⁺ or K⁺ cation; or M⁺ is an ammonium cation.
- 10
2. An oligonucleotide according to claim 1, wherein one of (A¹) and (A²) is a LNA nucleoside and the other one is a DNA nucleoside, a RNA nucleoside or a sugar modified nucleoside.
3. An oligonucleotide according to claim 1 or 2, wherein one of (A¹) and (A²) is a LNA nucleoside and the other one is a DNA nucleoside or a sugar modified nucleoside.
- 15
4. An oligonucleotide according to any one of claims 1 to 3, wherein one of (A¹) and (A²) is a LNA nucleoside and the other one is a DNA nucleoside.
5. An oligonucleotide according to any one of claims 1 to 3, wherein one of (A¹) and (A²) is a LNA nucleoside and the other one is a sugar modified nucleoside.
- 20
6. An oligonucleotide according to any one of claims 2 to 5, wherein said sugar modified nucleoside is a 2'-sugar modified nucleoside.
7. An oligonucleotide according to claim 6, wherein said 2'-sugar modified nucleoside is 2'-alkoxy-RNA, 2'-alkoxyalkoxy-RNA, 2'-amino-DNA, 2'-fluoro-RNA, 2'-fluoro-ANA or a LNA nucleoside.
- 25
8. An oligonucleotide according to claim 6 or 7, wherein said 2'-sugar modified nucleoside is a LNA nucleoside.

9. An oligonucleotide according to any one of claims 1 to 8, wherein the LNA nucleosides are independently selected from beta-D-oxy LNA, 6'-methyl-beta- D-oxy LNA and ENA.
10. An oligonucleotide according to claim 8 or 9, wherein the LNA nucleosides are both
5 beta-D-oxy LNA.
11. An oligonucleotide according to claim 6 or 7, wherein said 2'-sugar modified nucleoside is 2'-alkoxyalkoxy-RNA.
12. An oligonucleotide according to claim 9, wherein 2'-alkoxy-RNA is 2'-methoxy-RNA.
- 10 13. An oligonucleotide according to any one of claims 1 to 11, wherein 2'-alkoxyalkoxy-RNA is 2'-methoxyethoxy-RNA.
14. An oligonucleotide according to any one of claim 1 to 13, comprising between 1 and 15, in particular between 1 and 5, more particularly 1, 2, 3, 4 or 5 phosphorodithioate internucleoside linkages of formula (IA) or (IB) as defined in claim 1.
- 15 15. An oligonucleotide according to any one of claims 1 to 14, comprising further internucleoside linkages independently selected from phosphodiester internucleoside linkage, phosphorothioate internucleoside linkage and phosphorodithioate internucleoside linkage of formula (IA) or (IB) as defined in claim 1.
- 20 16. An oligonucleotide according to claim 15, wherein the further internucleoside linkages are independently selected from phosphorothioate internucleoside linkage and phosphorodithioate internucleoside linkage of formula (IA) or (IB) as defined in claim 1.
17. An oligonucleotide according to claim 15 or 16, wherein the further internucleoside linkages are all phosphorothioate internucleoside linkages.
- 25 18. An oligonucleotide according to claim 17 to 16, wherein the further internucleoside linkages are all phosphorodithioate internucleoside linkages of formula (IA) or (IB) as defined in claim 1.
19. An oligonucleotide according to any one of claims 1 to 18, wherein the oligonucleotide is of 7 to 30 nucleotides in length.
- 30 20. An oligonucleotide according to any one of claims 1 to 19, wherein one or more nucleoside is a nucleobase modified nucleoside.

21. An oligonucleotide according to any one of claims 1 to 20, wherein the oligonucleotide is an antisense oligonucleotide, a siRNA, a microRNA mimic or a ribozyme.
22. A pharmaceutically acceptable salt of an oligonucleotide according to any one of
5 claims 1 to 21, in particular a sodium or a potassium salt or ammonium salt.
23. A conjugate comprising an oligonucleotide or a pharmaceutically acceptable salt according to any one of claims 1 to 22 and at least one conjugate moiety covalently attached to said oligonucleotide or said pharmaceutically acceptable salt, optionally *via* a linker moiety.
- 10 24. A pharmaceutical composition comprising an oligonucleotide, pharmaceutically acceptable salt or conjugate according to any one of claims 1 to 23 and a therapeutically inert carrier.
25. An oligonucleotide, pharmaceutically acceptable salt or conjugate according to any one of claims 1 to 24 for use as a therapeutically active substance.
- 15 26. A process for the manufacture of an oligonucleotide according to any one of claims 1 to 21 comprising the following steps:
- (a) Coupling a thiophosphoramidite nucleoside to the terminal 5' oxygen atom of a nucleotide or oligonucleotide to produce a thiophosphite triester intermediate;
- (b) Thiooxidizing the thiophosphite triester intermediate obtained in step a); and
- 20 (c) Optionally further elongating the oligonucleotide.
27. An oligonucleotide manufactured according to a process of claim 26.
28. The invention as hereinbefore described.

FIGURES

Figure 1

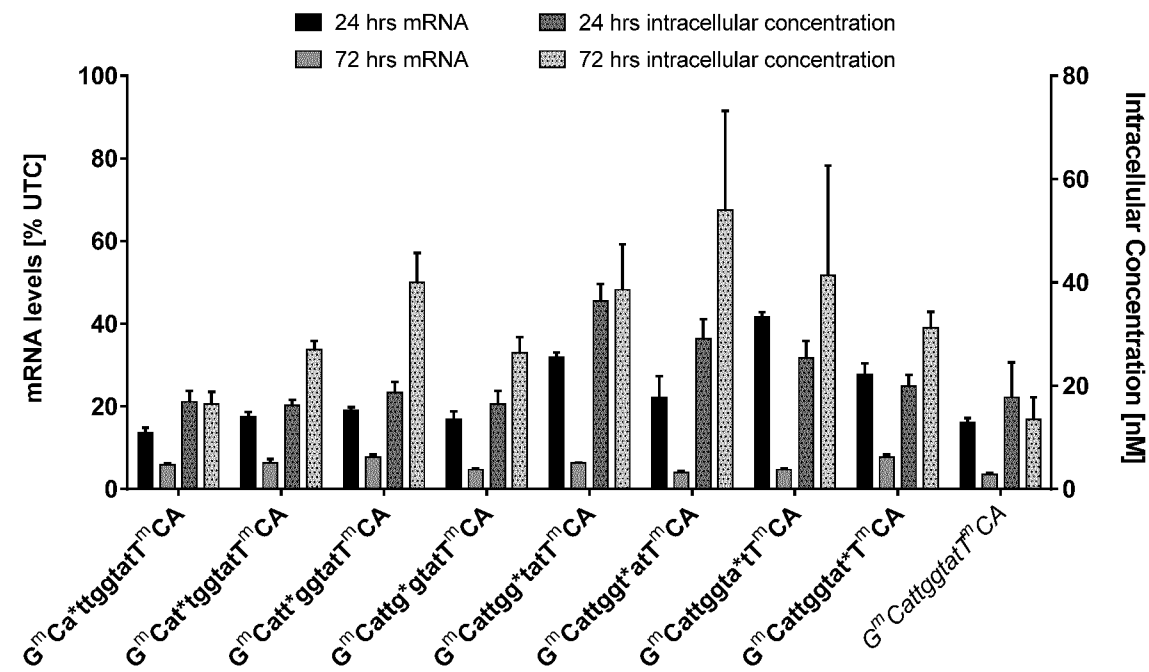


Figure 2

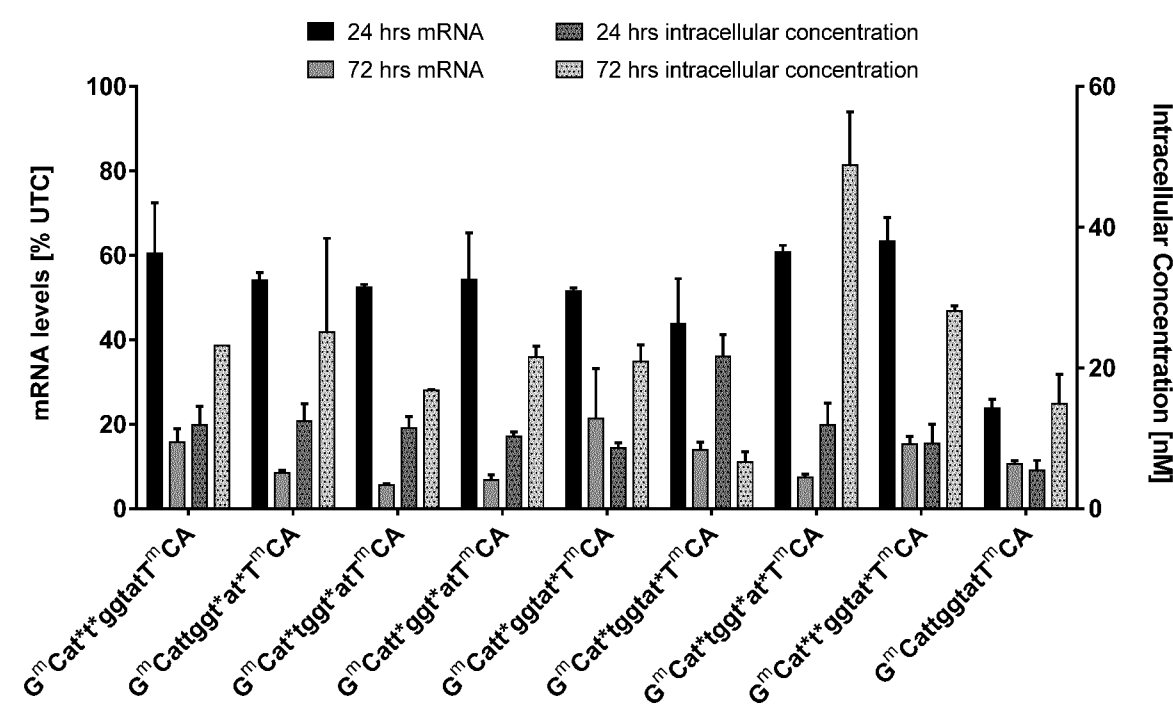


Figure 3

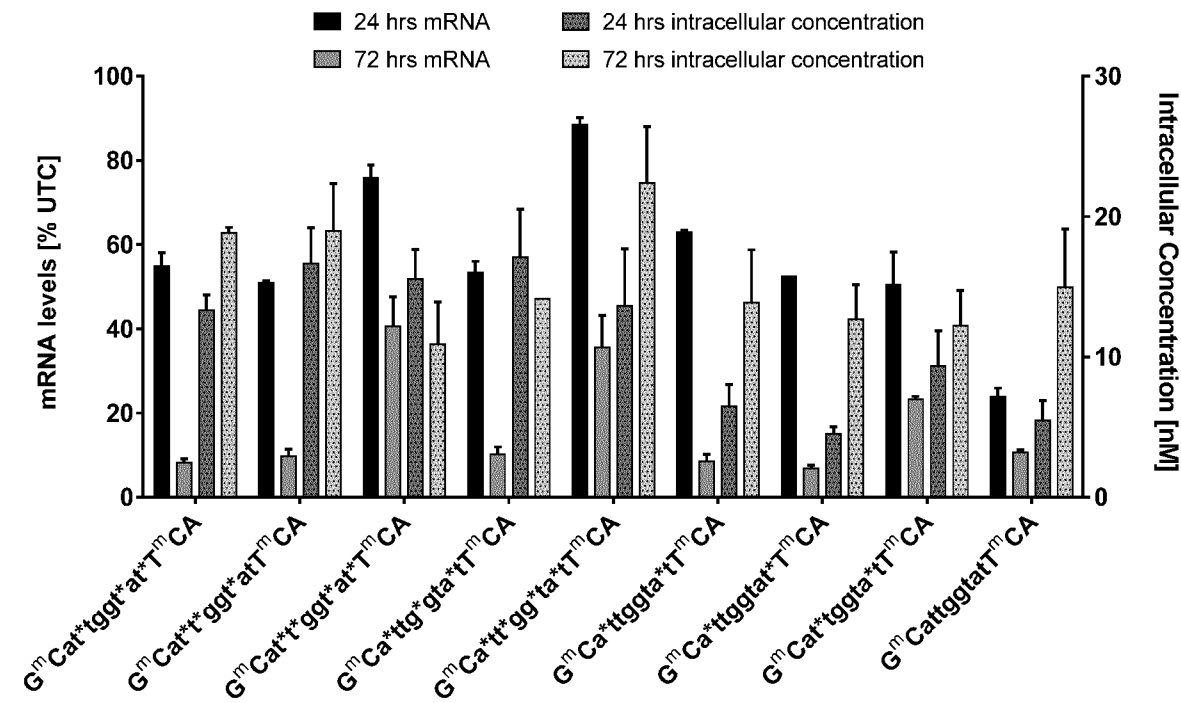


Figure 4

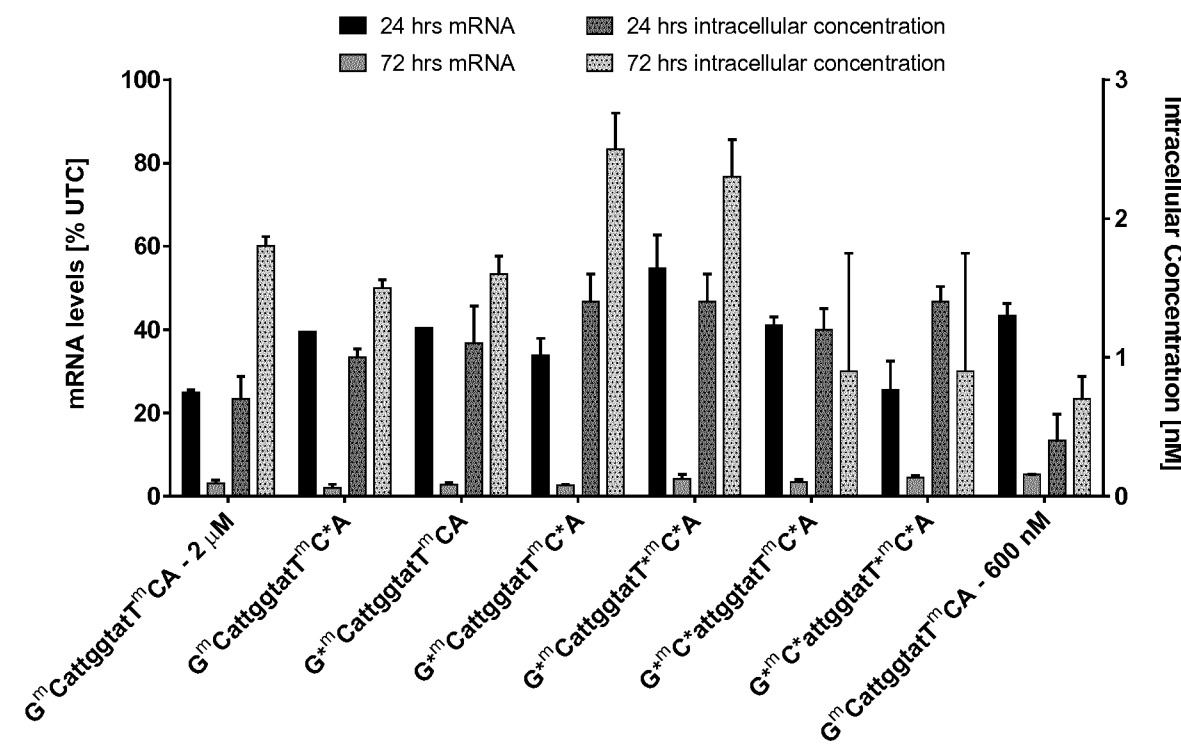


Figure 5

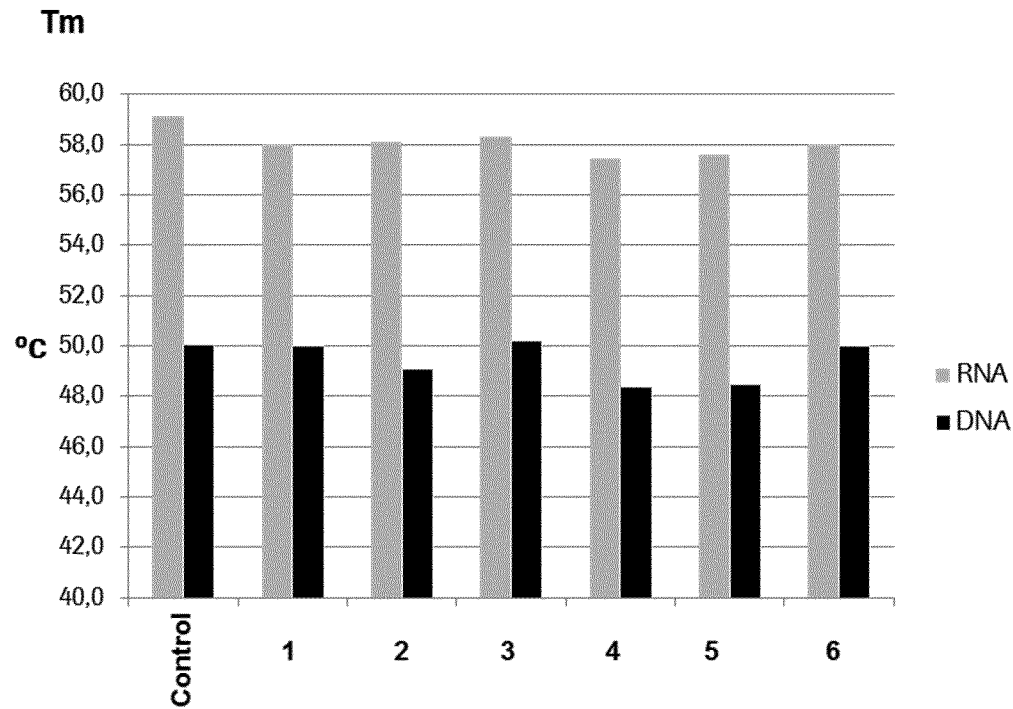


Figure 6

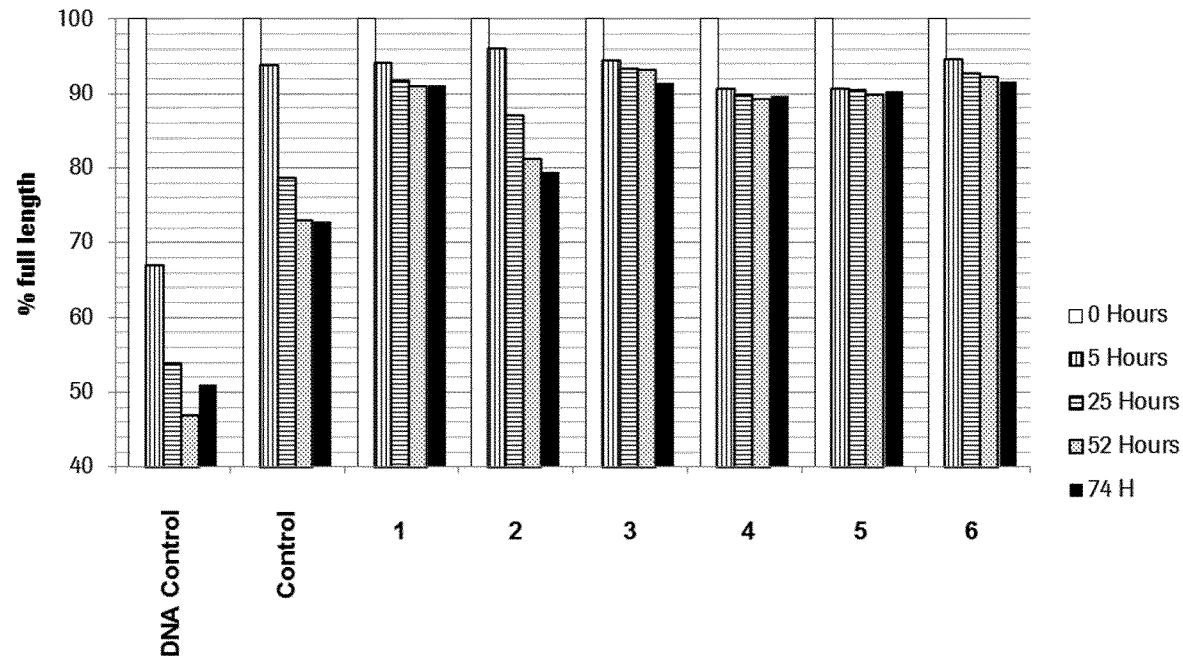


Figure 7

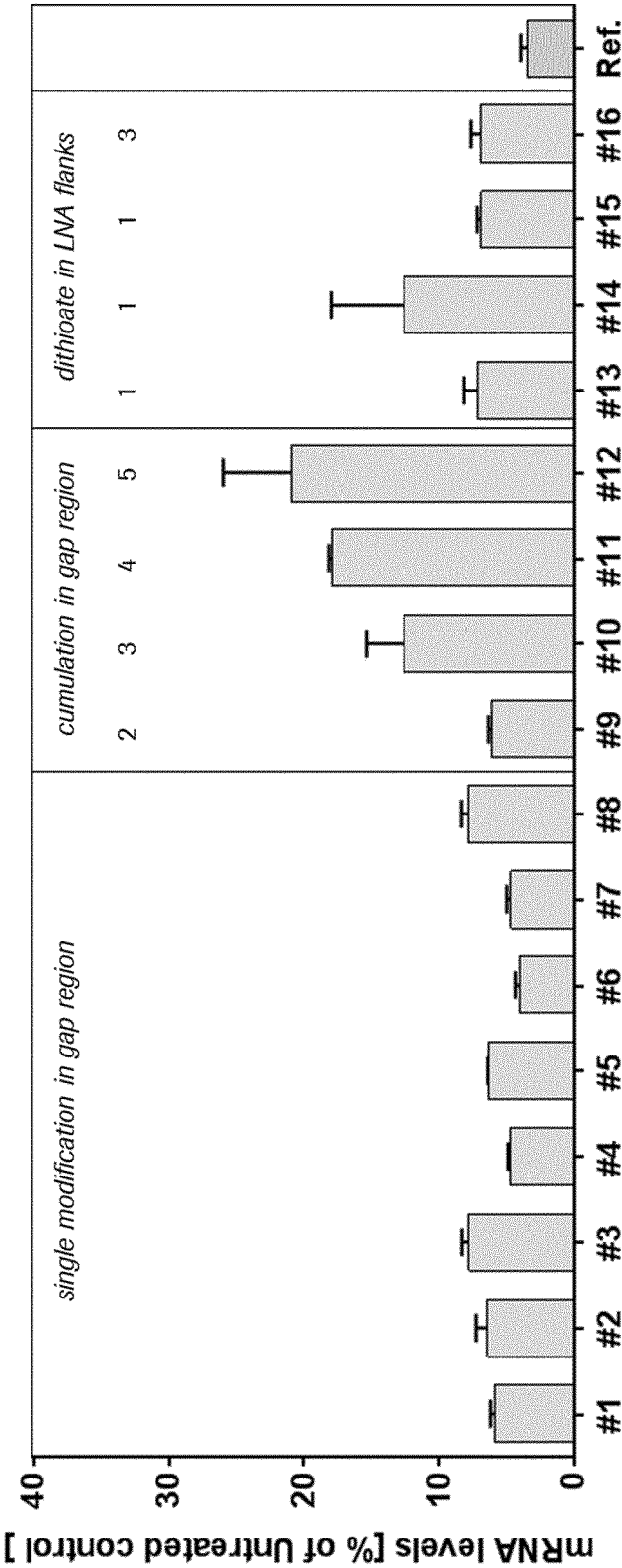


Figure 8

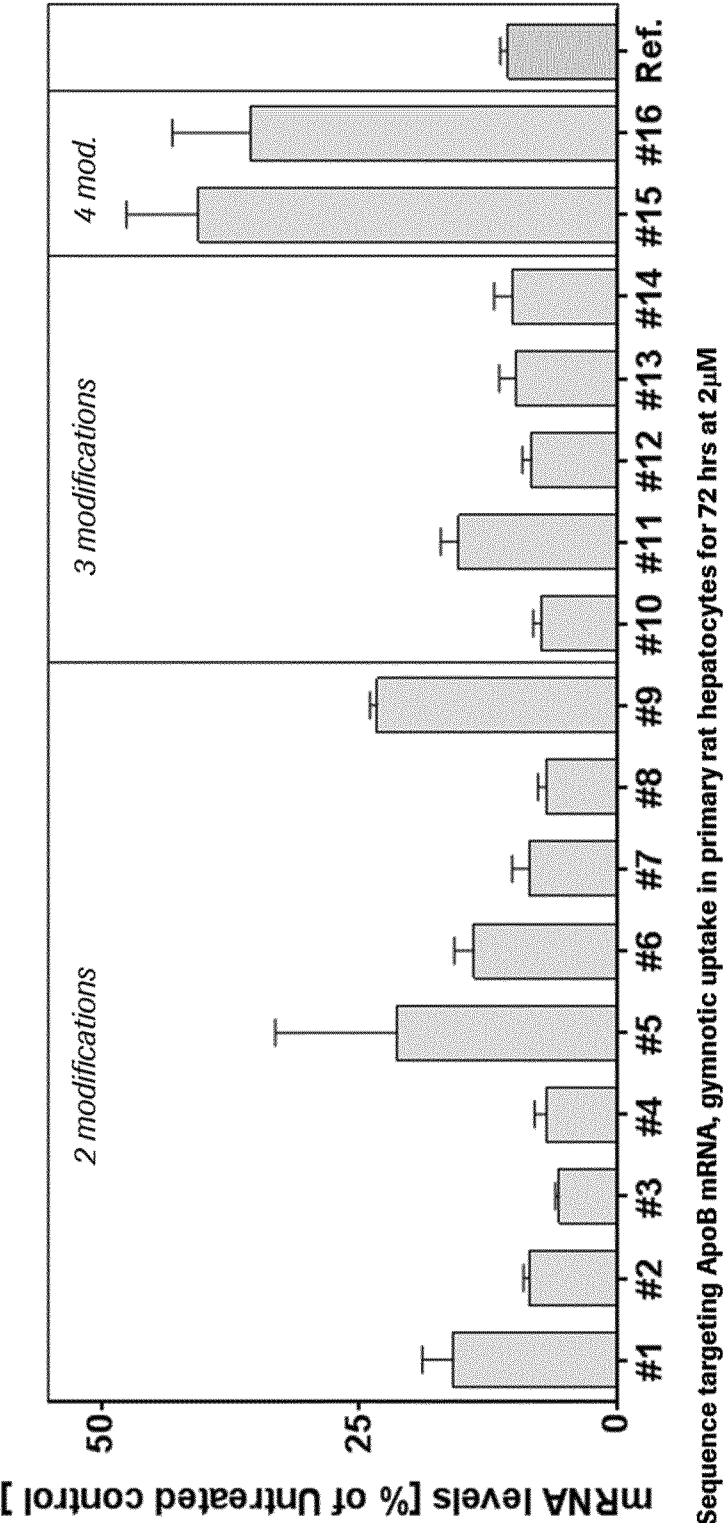


Figure 9A

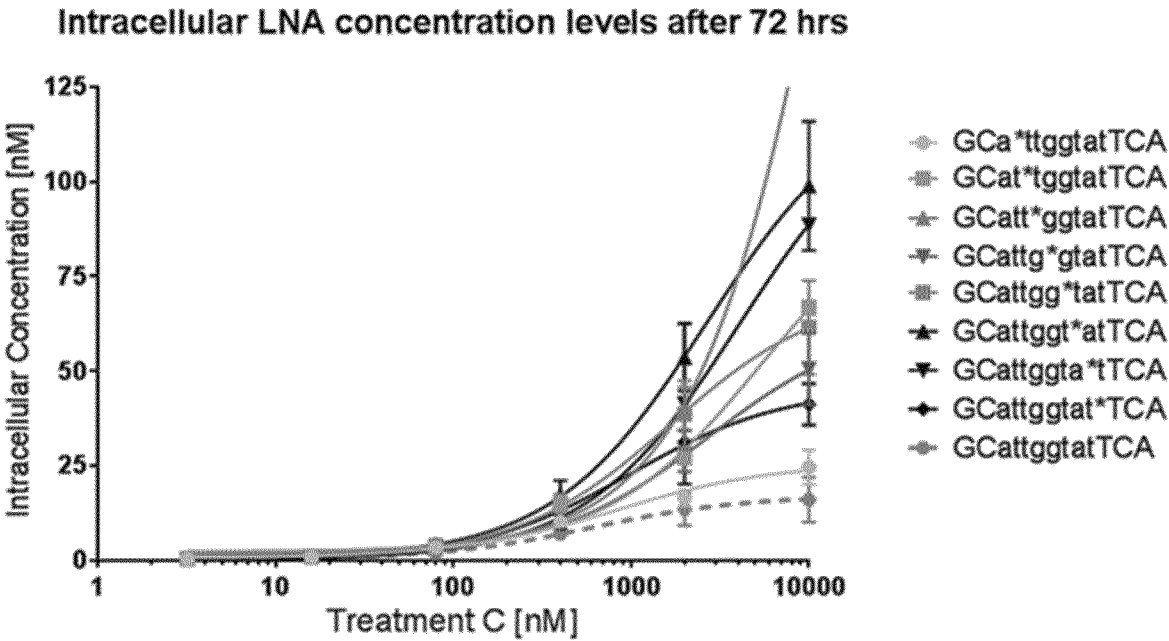


Figure 9B

Sequence	10 000nM ICC (nM)	2 000nM ICC (nM)	400nM ICC (nM)	80nM ICC (nM)	16nM ICC (nM)	3.2nM ICC (nM)	0.64nM ICC (nM)	0.128nM ICC (nM)
GCa*ttggatTCA	24.6	16.5	10.2	3.5	0.8	0.4	0.3	0.3
Gcat*tggtatTCA	66.7	27.0	14.9	3.4	1.0	0.4	0.4	0.3
Gcatt*ggatTCA	151.7	40.0	15.6	2.9	0.9	0.4	0.3	0.3
Gcattg*gtatTCA	50.6	26.4	11.9	3.8	0.9	0.3	0.2	0.2
GCattgg*atTCA	61.5	38.6	15.0	3.5	0.8	0.5	0.3	0.3
GCattggat*atTCA	98.9	53.6	17.3	4.1	1.1	0.6	0.4	0.3
GCattggga*tTCA	88.6	54.0	10.7	2.7	0.7	0.3	0.2	0.2
GCattgggtat*TCA	41.2	31.2	12.7	2.7	0.7	0.5	0.4	0.4
GCattgggtatTCA	16.0	13.5	6.9	1.7	0.5	0.3	0.2	0.2

Nomenclature:

G=LNA-G

a=DNA-A

*=non-bridging dithioate linkage

Figure 10A

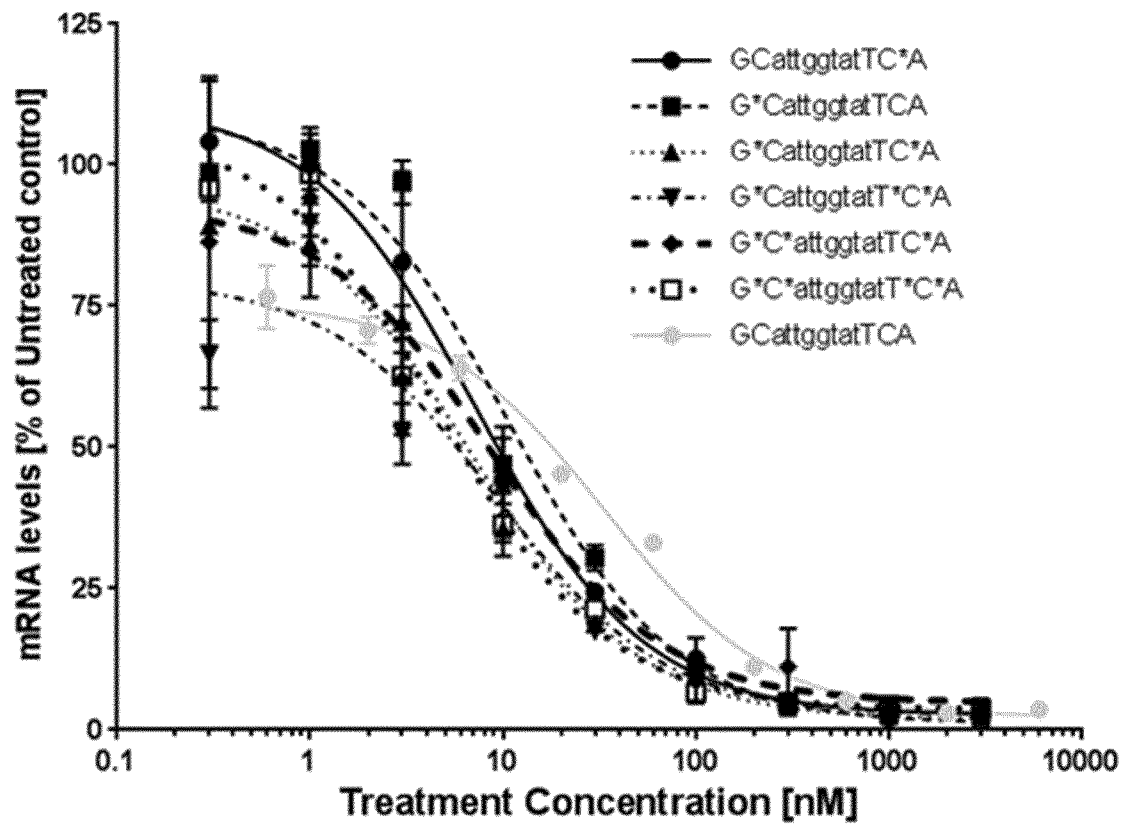


Figure 10B

Sequence	3000 nM mRNA (nM)	1000 nM mRNA (nM)	300 nM mRNA (nM)	100 nM mRNA (nM)	30 nM mRNA (nM)	10 nM mRNA (nM)	3 nM mRNA (nM)	1 nM mRNA (nM)	0.3 nM mRNA (nM)	0 nM mRNA (nM)
GCattggtatTC*A	2.97	2.01	4.89	12.65	24.49	44.07	82.75	99.86	104.26	101.40
G*CattggtatTCA	2.35	2.69	4.42	11.25	30.44	47.00	96.90	102.94	98.68	99.41
G*CattggtatTC*A	2.24	2.53	4.01	9.41	18.79	35.49	72.17	85.99	89.17	96.57
G*CattggtatT*C*A	3.90	4.10	4.44	8.62	17.46	43.47	52.39	89.74	66.49	100.90
G*C*attggtatTC*A	3.12	3.38	11.19	8.69	31.17	45.81	61.95	94.17	86.34	112.19
G*C*attggtatT*C*A	3.62	4.41	4.99	6.65	21.42	36.31	62.62	98.43	95.86	100.04
GCattggtatTCA	3.64	3.01	5.15	11.15	33.04	45.24	63.96	70.73	76.51	87.77

Nomenclature:

G=LNA-G

a=DNA-A

*=non-bridging dithioate linkage

Figure 11

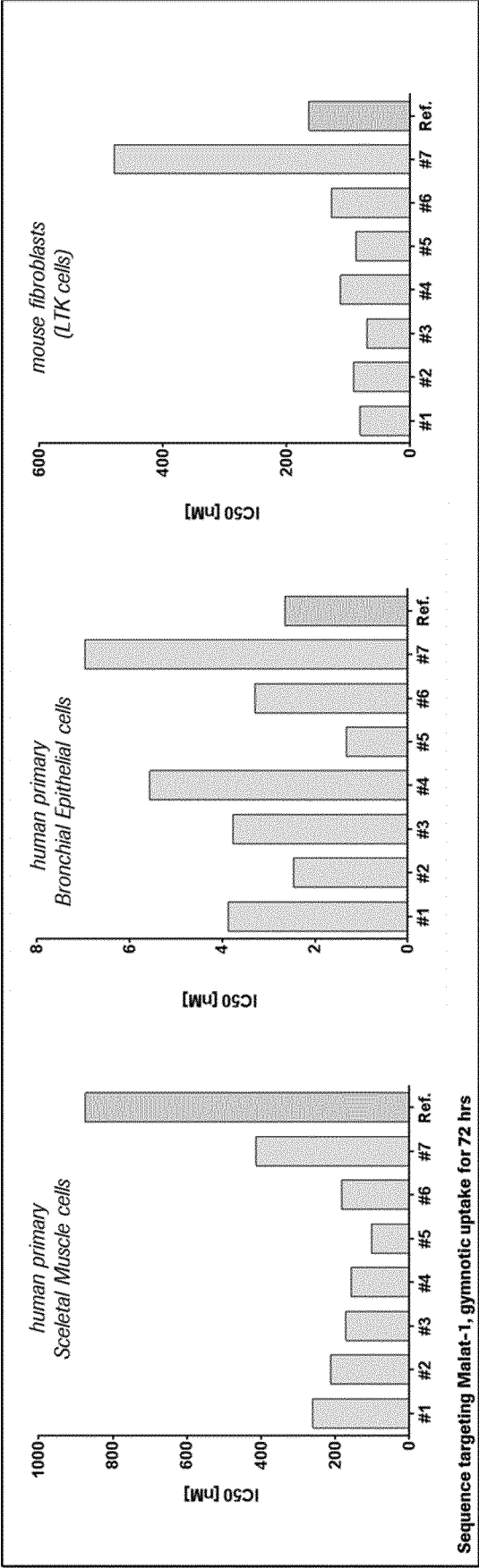


Figure 12

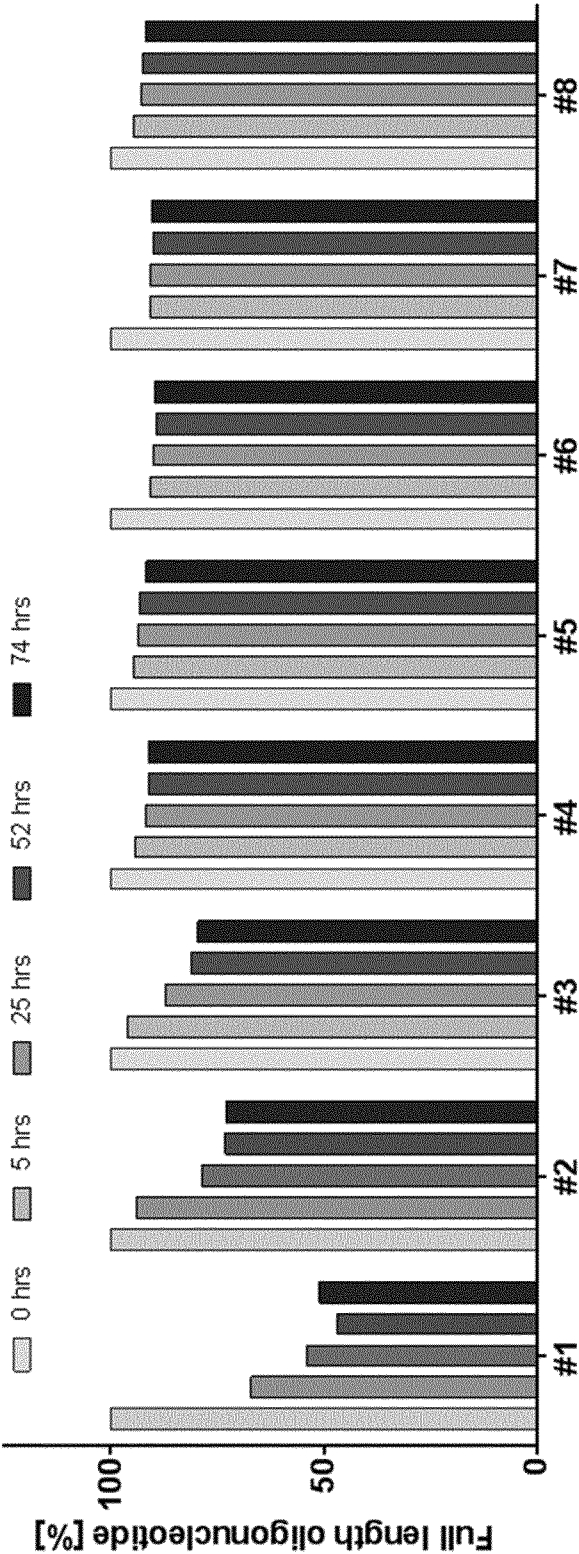


Figure 13

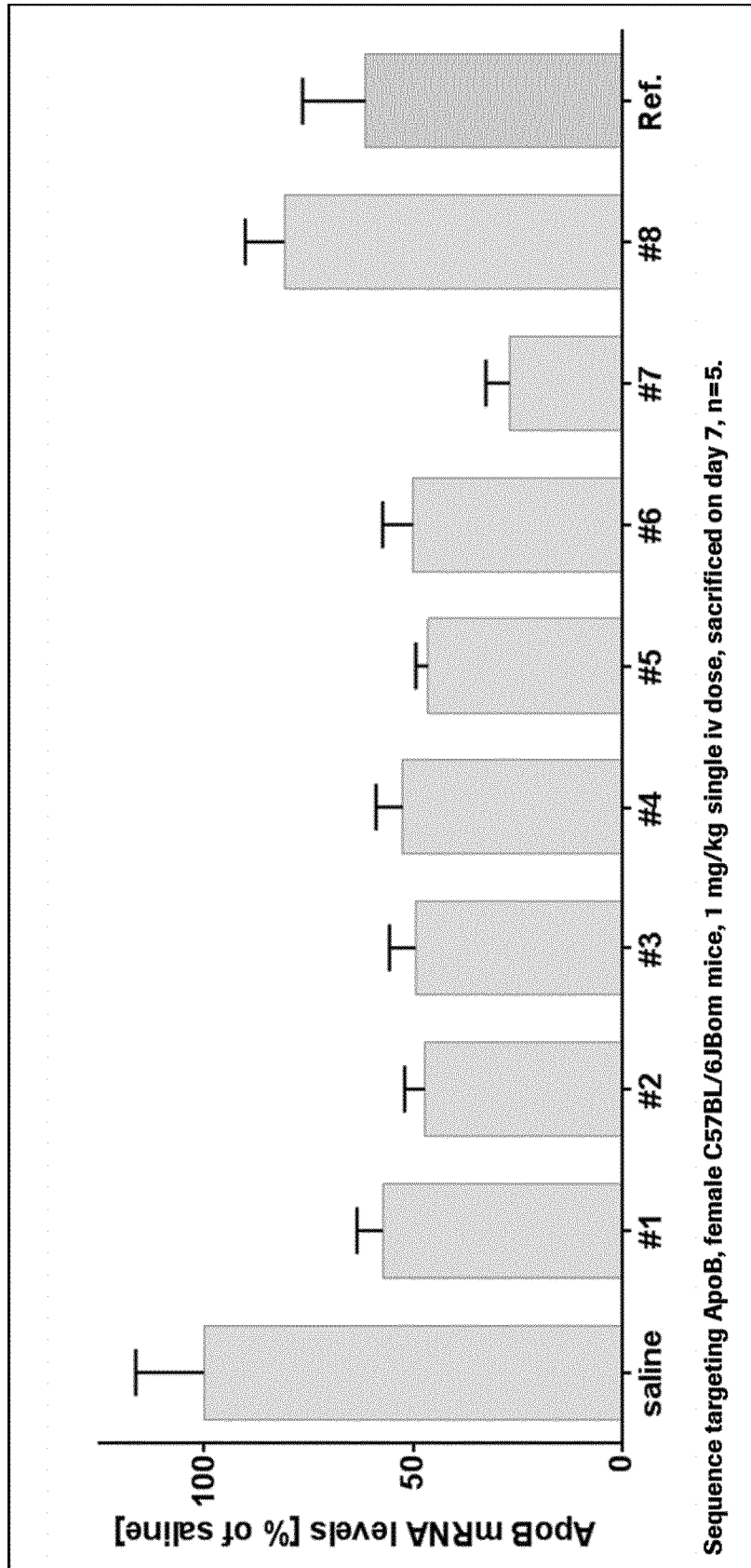


Figure 14A

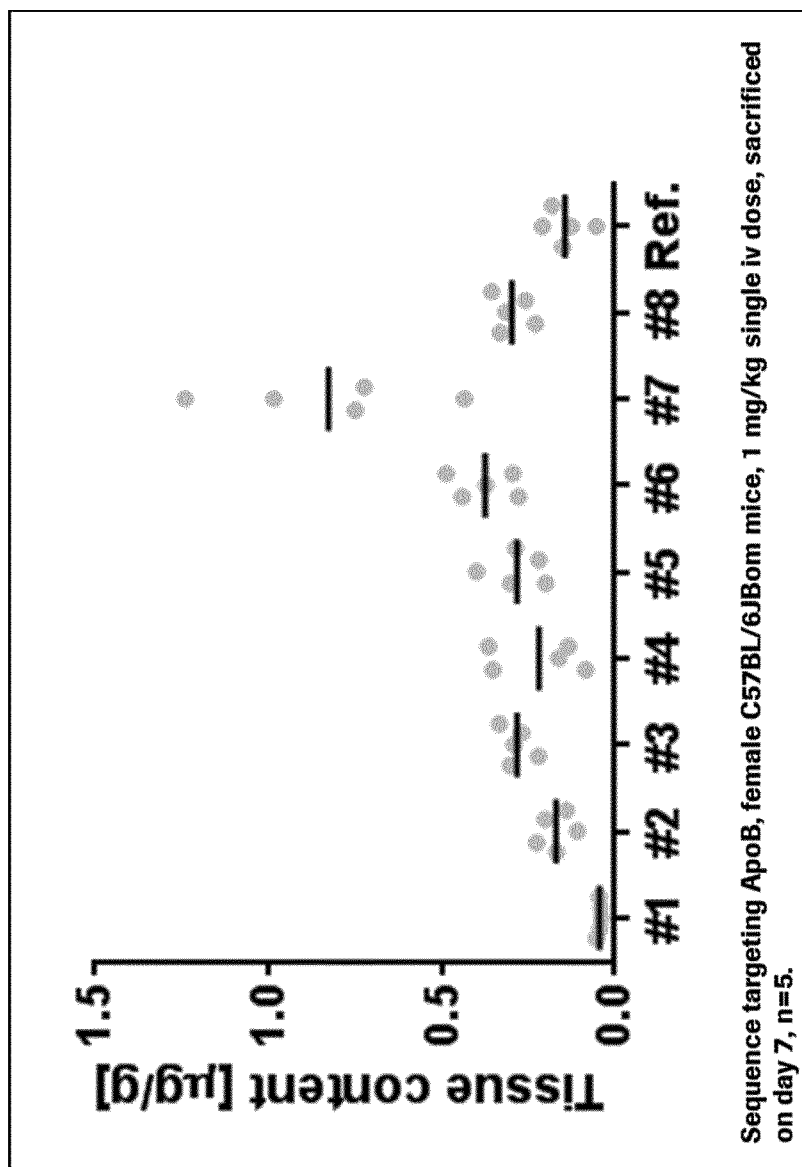


Figure 14B

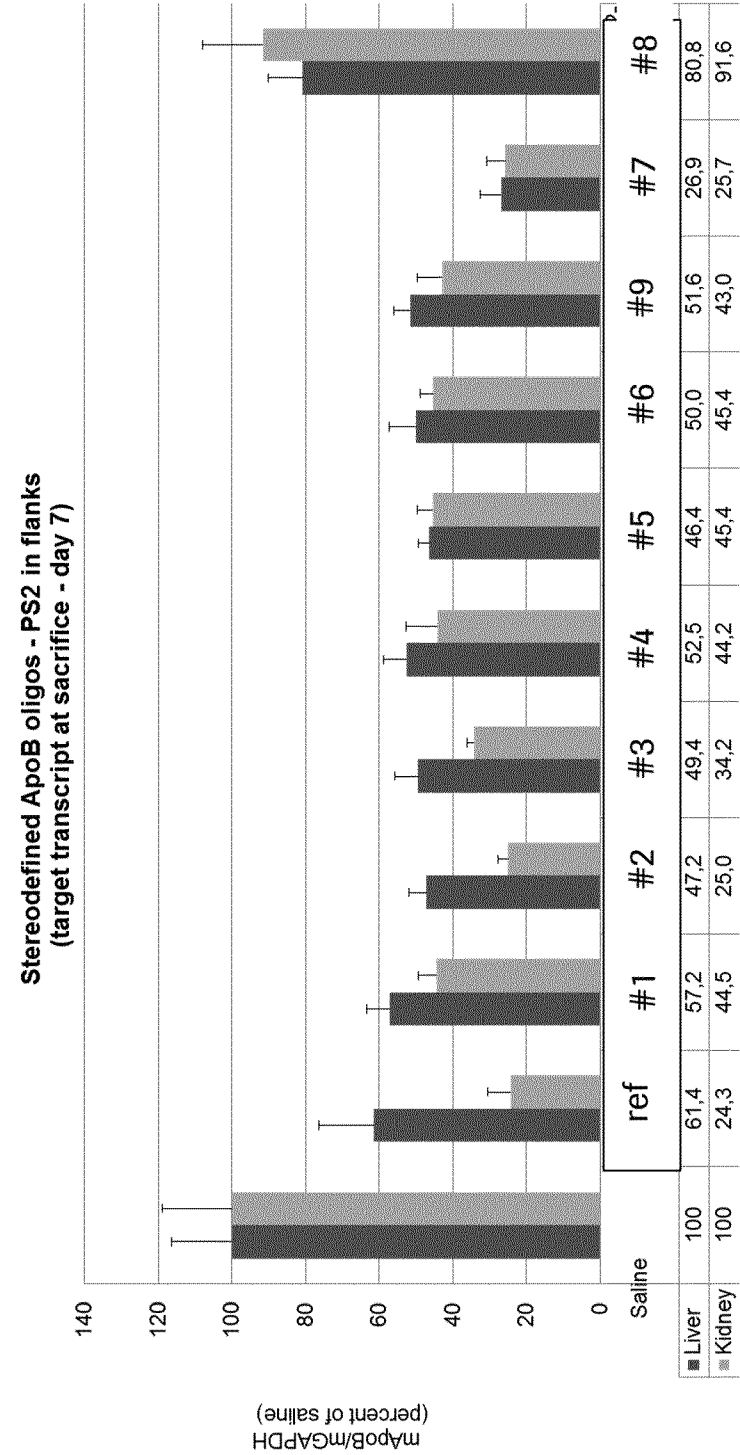


Figure 15A

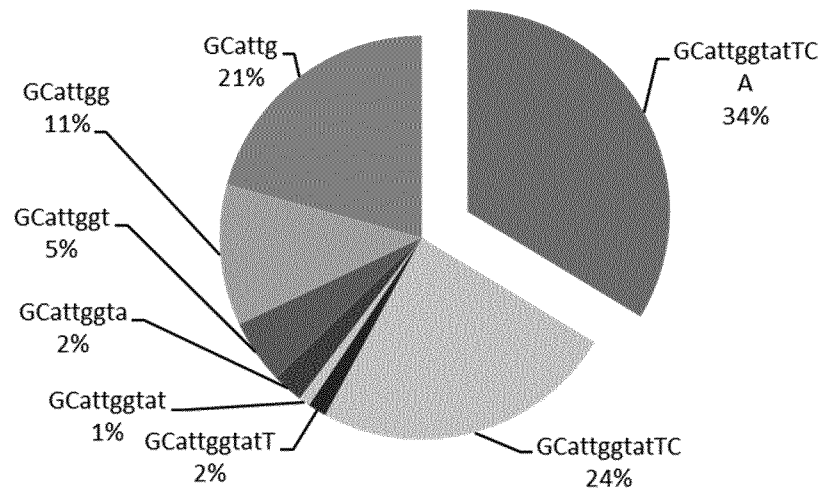
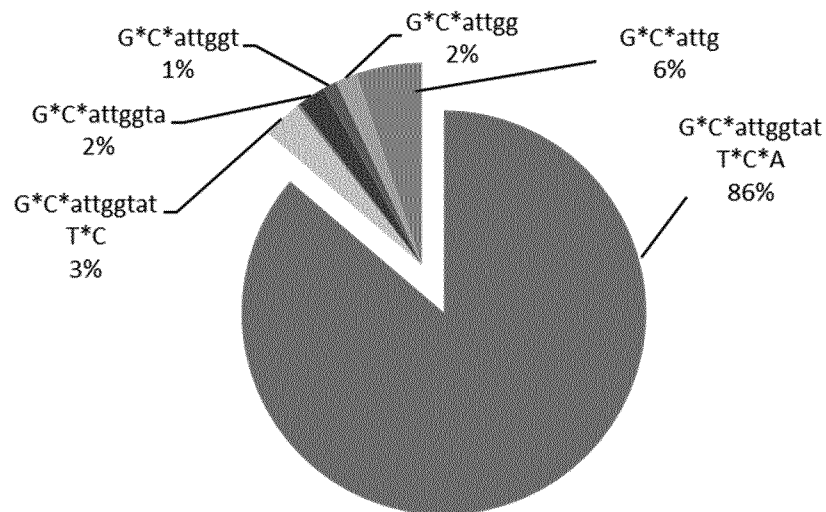
GCattggtatTCA**G*C*attggtatT*C*A**

Figure 15B

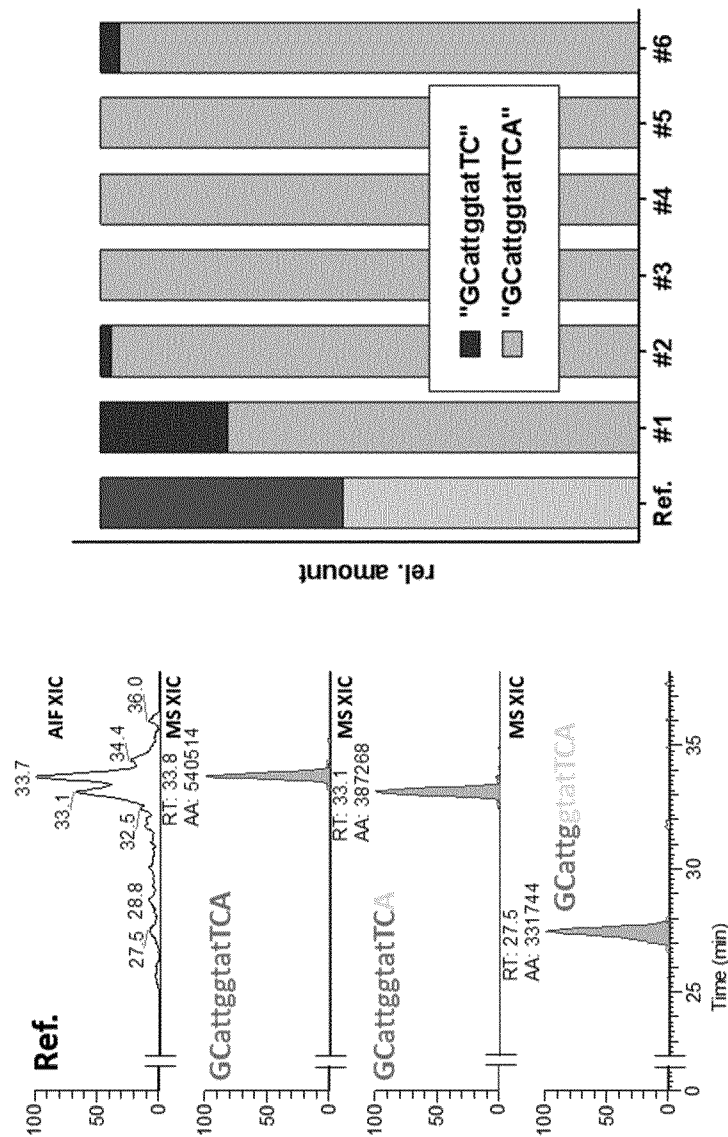


Figure 16

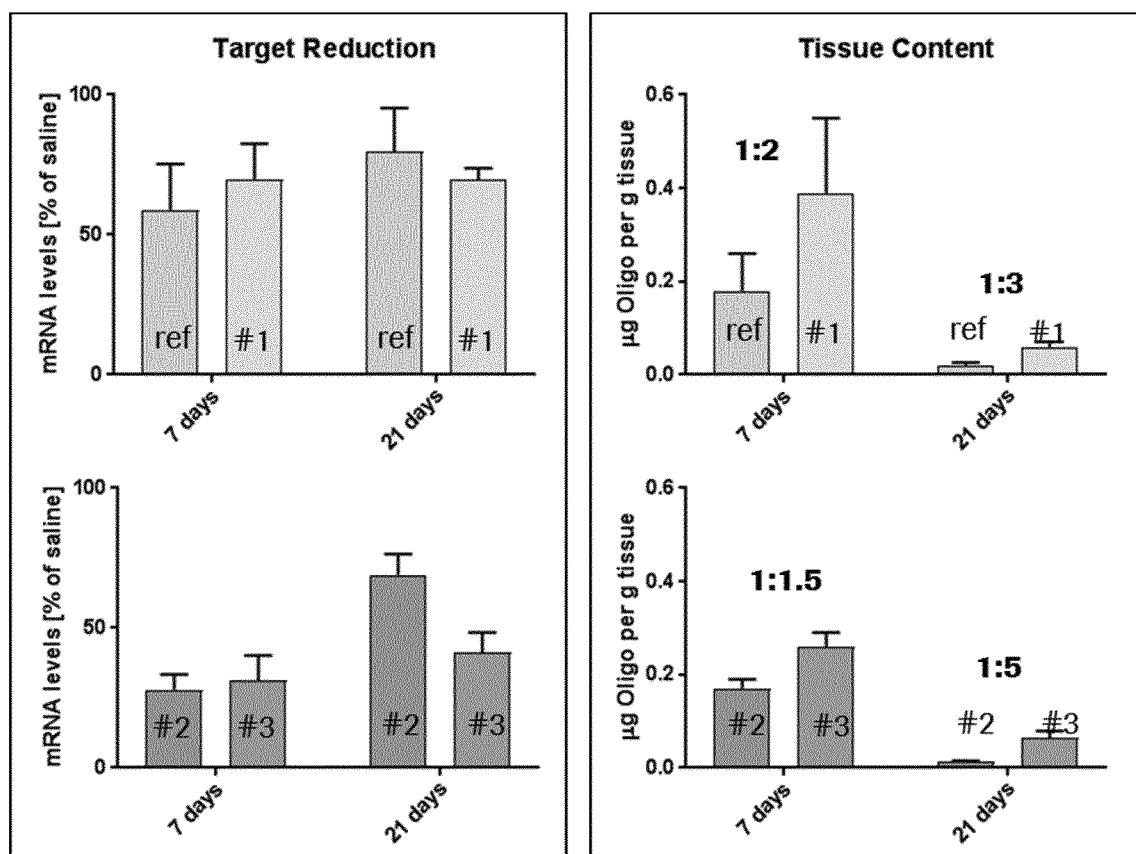
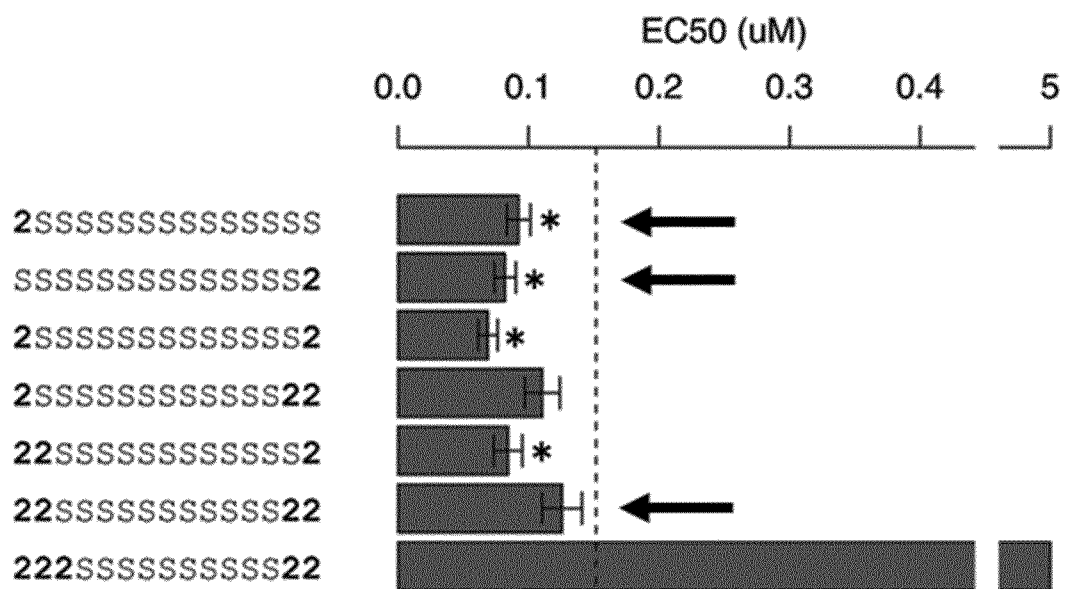


Figure 17A



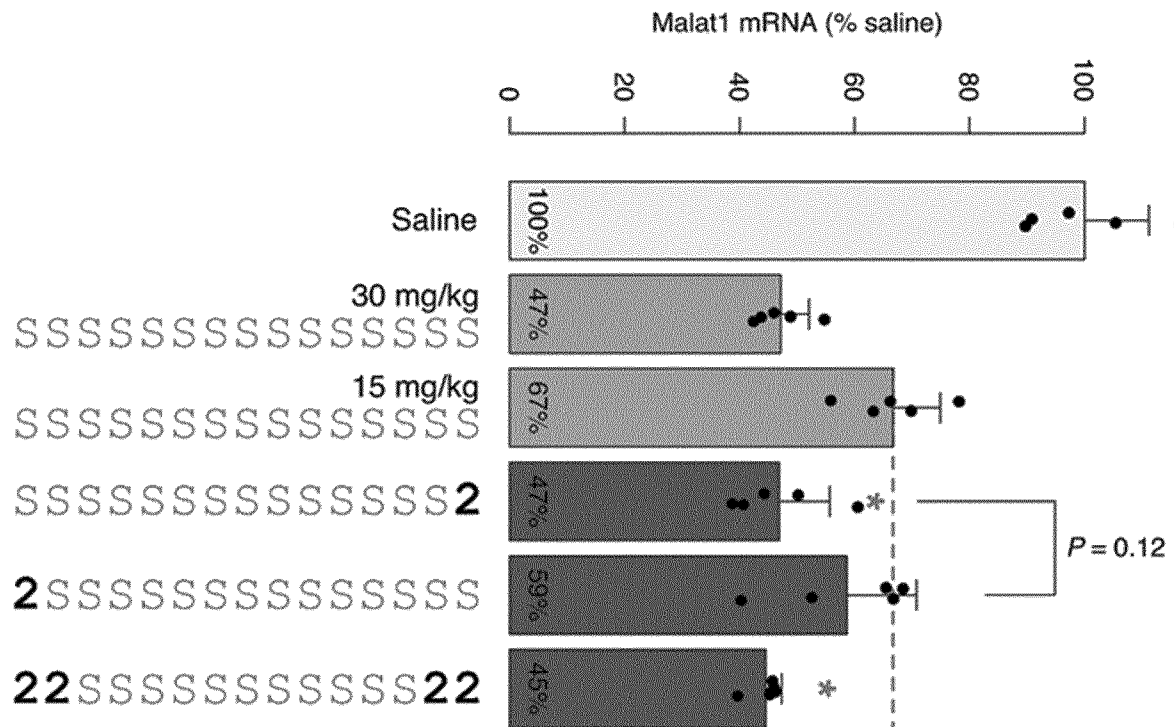


Figure 17C

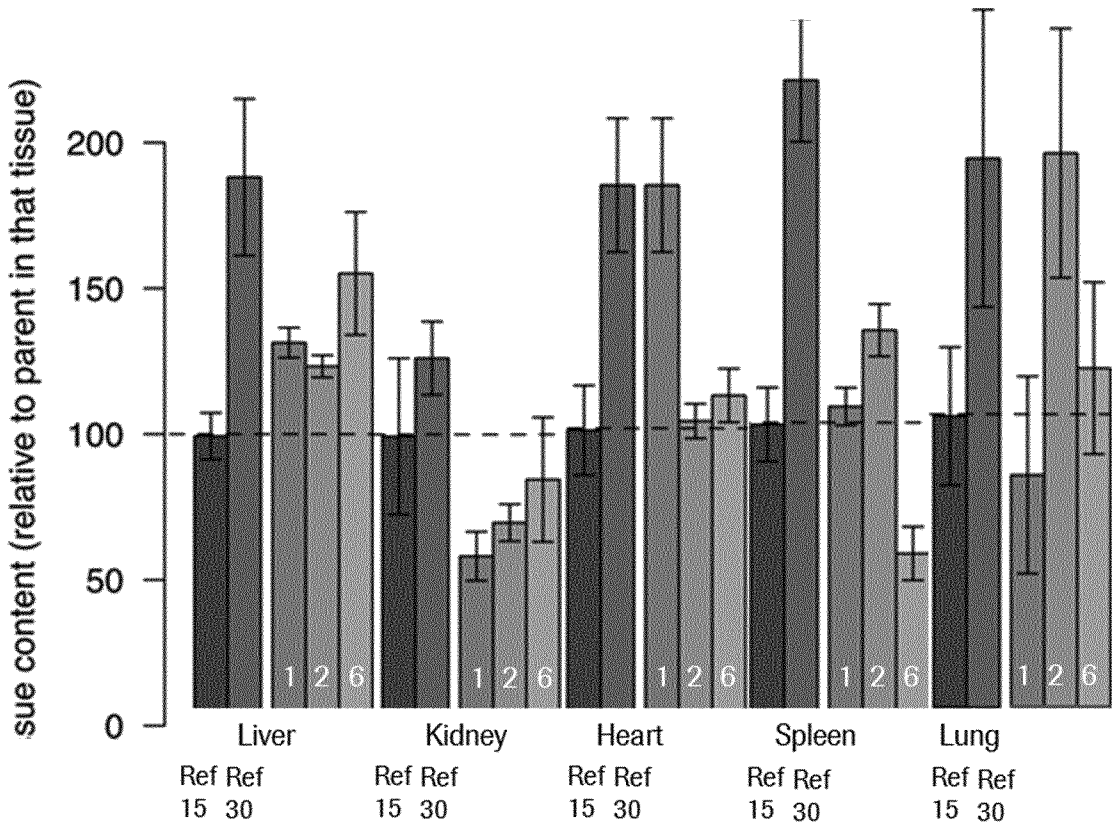


Figure 18A

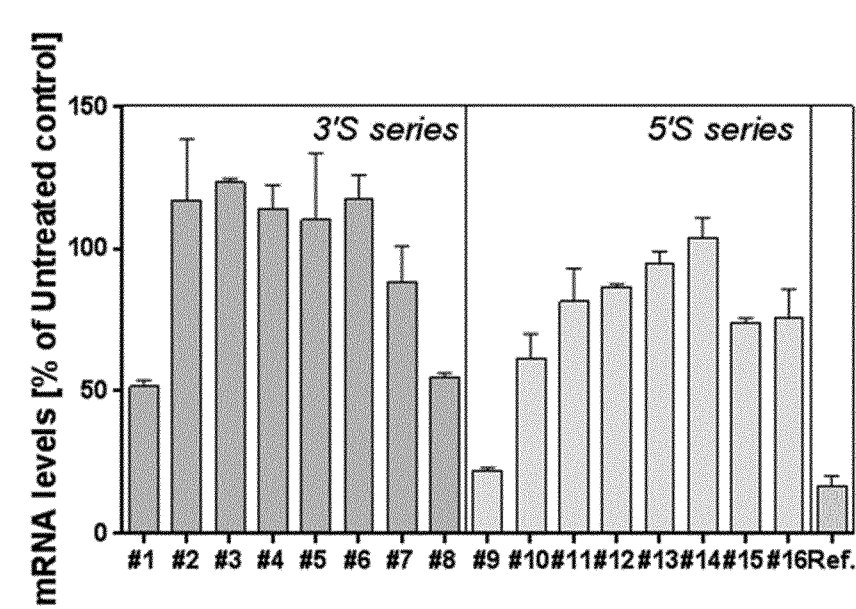


Figure 18B

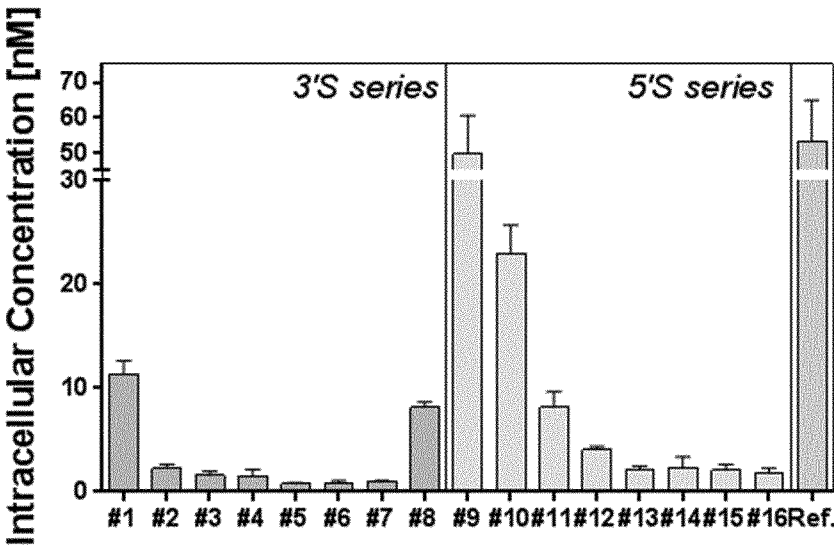


Figure 19A

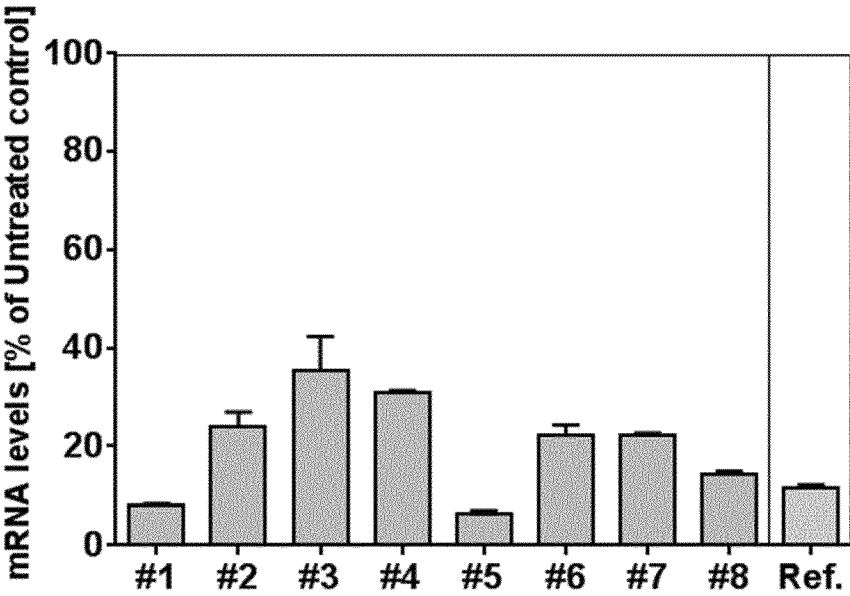


Figure 19B

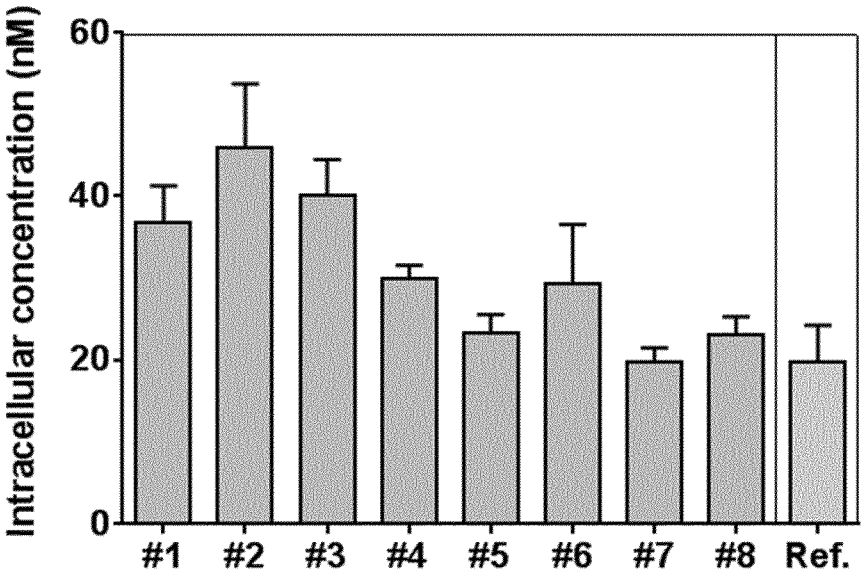


Figure 20

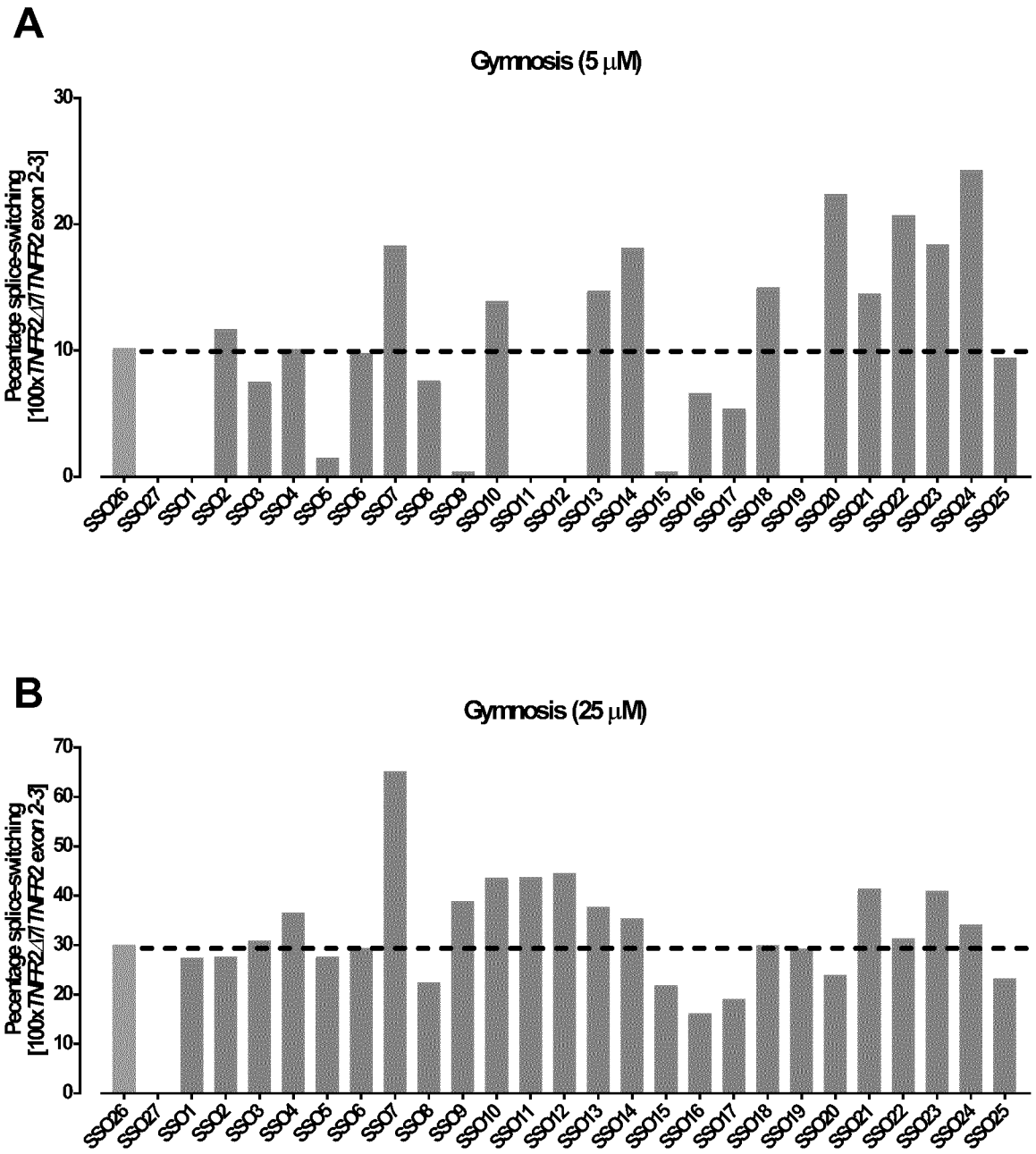
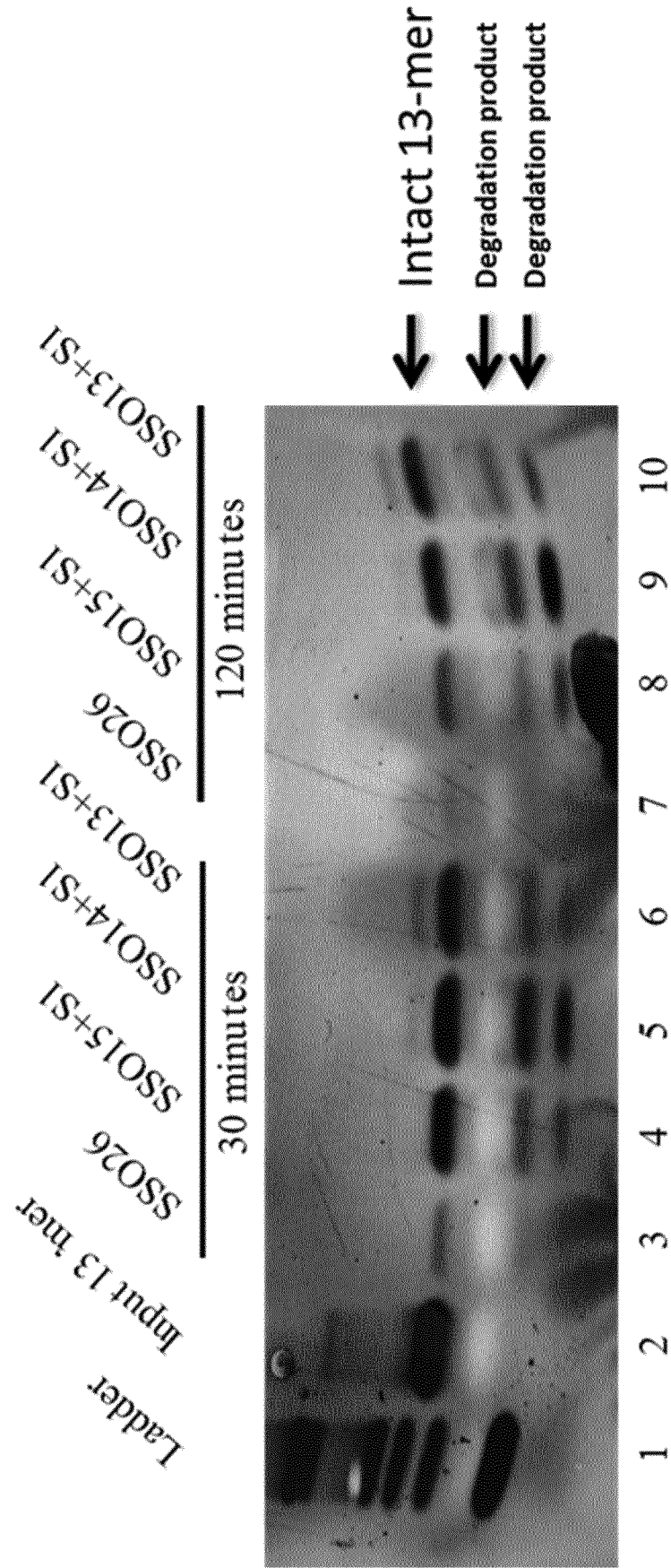


Figure 21



INTERNATIONAL SEARCH REPORT

International application No
PCT/EP2018/086460

A. CLASSIFICATION OF SUBJECT MATTER
INV. C12N15/11 C07F9/165 C07H19/10 C07H19/20 C07H21/00
ADD.

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
C12N C07F C07H

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

EPO-Internal, WPI Data, BIOSIS, EMBASE, CHEM ABS Data

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	US 2017/319614 A1 (HOSSBACH MARKUS [DE] ET AL) 9 November 2017 (2017-11-09) paragraph [0371] - paragraph [0372] paragraph [0411] - paragraph [0435]; claims 1,3,10; examples 27,32,139; tables 4-9 paragraph [0516] - paragraph [0536] paragraph [0831]	1-25,27,28
A	WO 2014/076195 A1 (SANTARIS PHARMA AS [DK]) 22 May 2014 (2014-05-22) claims 1,3	1-25,27,28
A	WO 2016/079183 A1 (ROCHE INNOVATION CT COPENHAGEN AS [DK]) 26 May 2016 (2016-05-26) page 43	1-25,27,28
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Further documents are listed in the continuation of Box C.



See patent family annex.

* Special categories of cited documents :

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier application or patent but published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art

"&" document member of the same patent family

Date of the actual completion of the international search

12 March 2019

Date of mailing of the international search report

17/05/2019

Name and mailing address of the ISA/

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Authorized officer

Bucka, Alexander

INTERNATIONAL SEARCH REPORT

International application No

PCT/EP2018/086460

C(Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	Xianbin Yang: "Solid-Phase Synthesis of Oligodeoxynucleotide Analogs Containing Phosphorodithioate Linkages : Synthesis of Oligodeoxynucleotide Analogs Containing PS2 Linkages" In: "Current Protocols in Nucleic Acid Chemistry", 1 September 2016 (2016-09-01), John Wiley & Sons, Inc., Hoboken, NJ, USA, XP055556956, ISBN: 978-0-471-14270-6 vol. 6614, pages 4.71.1-4.71.14, DOI: 10.1002/cpnc.13, the whole document -----	1-25,27, 28
A	SHERRY Y. WU ET AL: "2'-OMe-phosphorodithioate-modified siRNAs show increased loading into the RISC complex and enhanced anti-tumour activity", NATURE COMMUNICATIONS, vol. 5, no. 1, 12 March 2014 (2014-03-12), XP055566602, DOI: 10.1038/ncomms4459 the whole document -----	1-25,27, 28

INTERNATIONAL SEARCH REPORT

International application No.
PCT/EP2018/086460

Box No. II Observations where certain claims were found unsearchable (Continuation of item 2 of first sheet)

This international search report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☐ Claims Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:
3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box No. III Observations where unity of invention is lacking (Continuation of item 3 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see additional sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fees, this Authority did not invite payment of additional fees.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

1-25(completely); 27, 28(partially)

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest and, where applicable, the payment of a protest fee.
- ☐ The additional search fees were accompanied by the applicant's protest but the applicable protest fee was not paid within the time limit specified in the invitation.
- ☐ No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

1. claims: 1-25(completely); 27, 28(partially)

An oligonucleotide comprising at least one phosphorodithioate internucleoside linkage of formula (IA) or (IB) wherein one of the two oxygen atoms is linked to the 3' carbon atom of an adjacent nucleoside (A1) and the other one is linked to the 5'carbon atom of another adjacent nucleoside (A2), wherein at least one of the two nucleosides (A1) and (A2) is a LNA nucleoside and wherein in (IA) R is hydrogen or a phosphate protecting group, and in (IB) M⁺ is a cation, such as a metal cation, such as an alkali metal cation, such as a Na⁺ or K⁺ cation; or M⁺ is an ammonium cation.

2. claims: 26(completely); 27, 28(partially)

A process for the manufacture of an oligonucleotide according to any one of claims 1 to 21 comprising the following steps: (a) Coupling a thiophosphoramidite nucleoside to the terminal 5' oxygen atom of a nucleotide or oligonucleotide to produce a thiophosphite triester intermediate;(b) thiooxidizing the thiophosphite triester intermediate obtained in step a).

INTERNATIONAL SEARCH REPORT

Information on patent family members

International application No

PCT/EP2018/086460

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